GBS TOXIN RECEPTOR

INTRODUCTION

Technical Field

This invention provides compositions and methods relating to GBS toxin receptor polynucleotides and polypeptides. The invention relates to a receptor for a polysaccharide isolated from a bacterial source.

Background

Group B ß-hemolytic Streptococci (GBS) are ubiquitous microorganisms. GBS is not known to cause any harmful infections in humans except for very young babies. GBS pneumonia, also called "early-onset disease", is associated with high morbidity and mortality in newborn infants.

In a series of studies conducted by Dr. Carl G. Hellerqvist and his associates at the Vanderbilt University School of Medicine, Nashville, Tennessee, a polysaccharide GBS toxin was identified. This toxin was determined to be a major factor in the complications of GBS pneumonia, and was found to be useful as a therapeutic agent in combating tumors though inhibition of vascularization (U.S. Patent No. 5,010,062).

In addition, as described in U.S. Patent No. 5,858,991 and WO98/32453, GBS toxin facilitates wound healing in patients by minimizing scarring and accelerating healing, and reduces wound-related tumor progression.

WO98/32452 and WO98/32448 describe the use of GBS toxin as a therapeutic agent for treating patients with chronic inflammatory diseases, such as rheumatoid arthritis and psoriasis, and for enhancing repair of neural injury.

Prior to this invention, receptors for GBS toxin had not been identified. The inventors, believing receptors of GBS toxin to reside on cells in the developing vasculature of tissues undergoing angiogenesis in the conditions described above, embarked upon a series of experiments resulting in the present invention.

SUMMARY OF THE INVENTION

For the first time, novel receptors for group B β-hemolytic Streptococcus GBS toxin (GBS toxin receptor) have been identified. One aspect of the invention provides a polypeptide comprising a GBS toxin receptor or polypeptide fragment thereof. Preferred embodiments include mammalian GBS toxin receptors. Also provided is an antibody that recognizes GBS toxin receptor or a fragment thereof. The polypeptide of the invention can be used, *inter alia*, for the screening of compounds that can be used to treat or prevent conditions arising from pathologic or hypoxia-driven angiogenesis or neovascularization, such as, for example, cancerous tumors, chronic inflammatory disease, scarring during wound healing, keloids, neural injury, and reperfusion injury.

Another aspect of the invention provides a polynucleotide encoding a GBS toxin receptor or a fragment thereof and a polynucleotide hybridizable to such polynucleotide. Preferred polynucleotides are at least 10 bases in length and comprise a nucleic acid sequence encoding, or are complementary to a nucleic acid sequence encoding, a mammalian GBS toxin receptor or a polypeptide fragment thereof.

A third aspect of the invention is a complex comprising a GBS toxin bound to a mammalian toxin receptor or fragment thereof. Also provided is a method of forming such complex. The method comprises contacting a GBS toxin with a polypeptide comprising a mammalian GBS toxin receptor, or fragment thereof that can bind GBS toxin, under conditions that permit specific binding of the GBS toxin to the polypeptide, and allowing the complex to form.

Yet another aspect of the invention is a method for purifying a compound that binds a GBS toxin receptor. The method comprises providing a polypeptide comprising a mammalian GBS toxin receptor, or fragment thereof that binds GBS toxin, contacting the polypeptide with a sample comprising the compound under conditions that allow specific binding of the compound to the polypeptide, and separating the bound compound from the remainder of the sample.

Another aspect of the invention is a method of determining the presence or absence of GBS toxin in a sample. The method comprises contacting the sample with a polypeptide comprising a mammalian GBS toxin receptor, or fragment thereof that binds GBS toxin, under conditions that allow specific binding of GBS toxin to the GBS toxin receptor, and determining whether specific binding of GBS toxin has occurred. Presence of GBS toxin in a sample obtained from a neonate is indicative of early onset disease.

A sixth aspect of the invention is a method for detecting pathologic vasculature in a mammalian tissue. The method comprises detecting the presence of a GBS toxin receptor. The method can be used for detecting or monitoring a variety of medical conditions associated with angiogenesis or neovascularization, such as, for example, detecting metastasis of a cancerous tumor, or monitoring the

margin of a tumor in a mammal undergoing a therapy for cancer.

Another aspect of the invention provides methods for the identification of drug candidates for the treatment of medical conditions characterized by pathologic and/or hypoxia-driven angiogenesis or neovascularization. One embodiment is a method for identifying a compound that specifically binds a mammalian GBS toxin receptor. The method comprises combining a test compound with a mammalian GBS toxin receptor, or fragment thereof that can bind GBS toxin, under conditions that allow specific binding to occur, and detecting a complex formed between the test compound and the polypeptide. Another embodiment is a method for determining cytotoxicity of a test chimeric compound. The method comprises exposing a cell expressing a mammalian GBS toxin receptor, or fragment thereof that binds GBS toxin, to a test chimeric compound comprising a cytotoxic agent coupled to GBS toxin, and detecting signs of toxicity. Yet another embodiment is a method for identifying an inhibitor of a GBS toxin receptor by incubating test cells that express GBS toxin receptor, or a fragment thereof, in the presence and absence of a test compound and under conditions in which the cells incubated in the absence of the test compound can proliferate or migrate, and comparing the proliferation or migration of the test cells incubated in the presence and absence of the test compound, wherein less proliferation or migration in the presence of the test compound is indicative of the test compound being an inhibitor of the GBS toxin receptor. An inhibitor of endothelial cell proliferation or migration can be identified by the above method, wherein less proliferation or migration of test cells in the presence of the test compound is indicative of the test compound being an inhibitor of endothelial cell proliferation or migration. A therapeutic compound for the treatment or prevention of a medical condition characterized by pathologic angiogenesis or neovascularization can also be identified by the above method, wherein less proliferation or migration of test cells in the presence of the test compound is indicative of the test compound being a candidate therapeutic compound for the treatment or prevention of the medical condition.

The invention also provides a method for identifying a compound which inhibits binding of a GBS toxin to a mammalian GBS toxin receptor. The method comprises simulating and selecting the most probable conformations of a mammalian GBS toxin receptor, designing a chemically modified analog that substantially mimics the energetically most probable three-dimensional structure of the polypeptide, chemically synthesizing the analog, and evaluating the bioactivity of the analog. Also provided is a method for identifying a compound which binds to a mammalian GBS toxin receptor. The method comprises simulating and selecting the most probable conformations of a mammalian GBS toxin receptor, deducing the most probable binding domains of the polypeptide, designing a compound that would form the energetically most probable complexes with the polypeptide, chemically synthesizing the

compound, and evaluating the bioactivity of the compound.

Another aspect of the invention is a method for the prevention or treatment of neonatal onset disease in a human neonate by administering an inhibitor of binding of GBS toxin to a human GBS toxin receptor.

Yet another aspect of the invention is a method for inhibiting pathologic or hypoxia-driven endothelial cell proliferation or migration in a mammalian tissue. The method comprises specifically binding a molecule to a GBS toxin receptor present on the surface of at least one cell in the tissue, the molecule being selected from the group consisting of a compound that can evoke an inflammatory response when bound to a GBS toxin receptor in a mammal, a chimeric compound comprising a cytotoxic compound coupled to a compound that specifically binds the GBS toxin receptor, an inhibitor of GBS toxin receptor phosphorylation, and an inhibitor of GBS toxin receptor activity.

The invention also provides a GBS toxin receptor or fragment thereof, an inhibitor of a GBS toxin receptor, or an inhibitor of binding of a GBS toxin to a GBS toxin receptor, for use in a method of treatment of the human or animal body or for the manufacture of a medicament for the treatment of a medical condition characterized by pathologic or hypoxia-driven angiogenesis or neovascularization. Also provided is a chimeric compound comprising a cytotoxic agent coupled to a compound that binds GBS toxin receptor for use in a method of treatment of the human or animal body.

Also provided are pharmaceutical compositions comprising an inhibitor of a GBS toxin receptor and/or a chimeric compound comprising a cytotoxic agent coupled to a compound that binds GBS toxin receptor, and a pharmaceutically acceptable carrier.

The invention also provides kits comprising a GBS toxin receptor or fragment and/or reagents for detecting the presence of a GBS toxin receptor or polypeptide fragment thereof or the presence of a polynucleotide encoding same.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 depicts a process of rational drug design.

FIGS. 2A and **2B** depict the results of immunohistochemical analysis of GBS toxin receptor expression in cancerous and normal human ovary tissue, respectively, using antibody Pab55 as described in Example 4.

FIGS. 3A and **3B** depict the results of immunohistochemical analysis of GBS toxin receptor expression in cancerous and normal human ovary tissue, respectively, using antibody Pab57 as described in Example 4.

FIGS. 4A-4C depict the targeted delivery of a chimeric compound to GBS toxin receptor expressed in a cancerous tissue as described in Example 6.

DESCRIPTION OF SPECIFIC EMBODIMENTS

DEFINITIONS

Generally, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. The nomenclature used herein and the laboratory procedures in cell culture, molecular genetics, and nucleic acid chemistry and hybridization described below are those well known and commonly employed in the art. Standard techniques are used for recombinant nucleic acid methods, polynucleotide synthesis, and microbial culture and transformation (e.g., electroporation, lipofection). Enzymatic reactions and purification steps supplied by manufacturers are typically performed according to the manufacturer's specifications. The techniques and procedures are generally performed according to conventional methods in the art and various general references (*See* generally, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2d ed. (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.) which are provided throughout this document. The nomenclature used herein and the laboratory procedures in analytical chemistry, organic synthetic chemistry, and pharmaceutical formulation described below are those well known and commonly employed in the art. Standard techniques can be used for chemical syntheses, chemical analyses, pharmaceutical formulation and delivery, and treatment of patients. As employed throughout the disclosure, the following terms, unless otherwise indicated, shall be understood to have the following meanings:

By "GBS toxin receptor" is meant a proteinaceous molecule capable of binding a toxin from Group B β-hemolytic *Streptococcus* bacteria (GBS toxin), such as, for example, CM101. A GBS toxin receptor is usually found in nature on the surface of a cell. Recombinant membrane bound and soluble GBS toxin receptors can be produced by laboratory techniques known in the art and described herein.

The term "isolated polynucleotide" referred to herein means a polynucleotide that has been subjected to manipulation, such that the isolated polynucleotide is no longer associated with the chromosome or cell that the polynucleotide is normally associated with in nature in the same manner as it is normally associated in nature. An example of an "isolated polynucleotide" is a polynucleotide of genomic, recombinant, or synthetic origin or some combination thereof.

The term "isolated protein" referred to herein means a protein that is no longer associated with the cell that the protein is normally associated with in nature in the same manner as it is normally associated in nature, such as (1) a protein free of at least some other proteins from the same source, (2) a

protein expressed by a cell from a different species, (3) a protein that does not occur in nature, and (4) a protein produced from cDNA, recombinant RNA, or synthetic origin or some combination thereof.

The term "polypeptide" is used herein as a generic term to refer to native protein, fragments, or analogs of a polypeptide sequence. Hence, native protein, fragments, and analogs are species of the polypeptide genus.

The term "naturally occurring" means found in nature. For example, a polypeptide or polynucleotide sequence that is present in an organism (including viruses) found in nature and which has not been intentionally modified by man in the laboratory is naturally-occurring.

The term "operably linked" refers to a juxtaposition wherein the components so described are in a relationship permitting them to function in their intended manner. A control sequence "operably linked" to a coding sequence is ligated in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequences.

The term "control sequence" refers to polynucleotide sequences which are necessary to effect the expression of coding sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism; in prokaryotes, such control sequences generally include promoter, ribosomal binding site, and transcription termination sequence; in eukaryotes, generally, such control sequences include promoters and transcription termination sequence. The term "control sequences" is intended to include, at a minimum, all components whose presence is necessary for expression, and can also include additional components whose presence is advantageous, for example, leader sequences and fusion partner sequences.

The term "polynucleotide" as referred to herein means a polymeric form of nucleotides of at least 10 bases in length, either ribonucleotides or deoxyribonucleotides or a modified form of either type of nucleotide. The term includes single- and double-stranded forms of DNA.

The term "oligonucleotide" referred to herein includes naturally occurring, and modified nucleotides linked together by naturally occurring and non-naturally occurring oligonucleotide linkages. An oligonucleotide is usually a polynucleotide 200 bases or fewer in length. Preferably oligonucleotides are minimally 10 to 60 bases in length and most preferably
15-35 bases in minimal length. Oligonucleotides are usually single-stranded, e.g. for probes; although oligonucleotides may be double-stranded, e.g. for use in the construction of a gene mutant. Oligonucleotides of the invention can be either sense or antisense oligonucleotides. The term "naturally occurring nucleotides" referred to herein includes deoxyribonucleotides and ribonucleotides. The term "modified nucleotides" referred to herein includes nucleotides with modified or substituted sugar groups and the like. The term "oligonucleotide linkages" referred to herein includes oligonucleotides linkages

such as phosphorothioate, phosphorodithioate, phosphoroselenoate, phosphorodiselenoate, phosphoroanilothioate, phoshoraniladate, phosphoroamidate, and the like. An oligonucleotide can include a label for detection, if desired.

By "complementary" or "complement" is meant that wherever adenine appears in a first nucleic acid sequence, thymine or uracil is found in the "complementary" sequence and vice versa, and wherever guanine appears in a first nucleic acid sequence, cytosine is found in the "complementary" sequence and vice versa.

The term "sequence identity" describes the proportion of base matches between two nucleic acid sequences or the proportion of amino acid matches between two amino acid sequences, i.e. the degree of identity between two sequences. When sequence identity is expressed as a percentage, e.g., 50%, the percentage denotes the proportion of exact matches over the length of sequence from a GBS toxin receptor sequence that is compared to some other sequence. Various computer alignment programs can be used to determine sequence identity. In its simplest form, % identity is calculated by dividing the number of exact matches between two nucleic acid sequences or between two amino acid sequences by the total number of nucleotides or amino acids in the reference sequence. For example, if there are 300 matches between sequences 400 amino acids in length, the sequences have 75% identity. Uracil and thymine are considered identical when comparing a ribonucleic acid sequence with a deoxyribonucleic acid sequence.

As applied to polynucleotides, the term "substantial identity" means that two nucleic acid sequences when optimally aligned, such as by the program BLAST (Altschul et al., *J. Mol. Biol.* **215**:403-410 (1990)), share at least about 85%, preferably at least about 90% sequence identity and most preferably 95% or greater sequence identity. When using computer alignment programs, gaps (in either of the two sequences) are permitted to maximize matching; gap lengths of 15 bases or less are usually used; 6 bases or less are preferred; 2 bases or less are most preferred. When using oligonucleotides as probes or in treatments, the sequence identity between the target nucleic acid and the oligonucleotide sequence is generally not less than 17 target base matches out of 20 possible oligonucleotide base pair matches (85%); preferably not less than 9 matches out of 10 possible base pair matches (90%), and most preferably not less than 19 matches out of 20 possible base pair matches (95%).

Preferably, bases which are not identical nevertheless are part of a degenerate codon that encodes the same amino acid at that amino acid position. Alternatively, bases which are not identical preferably are part of a degenerate codon that encodes a conservative amino acid substitution for that amino acid position.

As applied to polypeptides, the term "substantial identity" means that two peptide sequences,

when optimally aligned by the BLAST computer program, share at least about 80 percent sequence identity, preferably at least about 86 percent sequence identity, more preferably at least about 95 percent sequence identity, even more preferably at least about 99 percent sequence identity up to having one amino acid difference, and most preferably share 100% identity. Gaps (in either of the two sequences being matched) are allowed in maximizing matching; gap lengths of 5 or less are preferred with 2 or less being more preferred. Preferably, residue positions which are not identical differ by conservative amino acid substitutions. Conservative amino acid substitutions refer to the interchangeability of residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Preferred conservative amino acid substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, glutamic-aspartic, and asparagine-glutamine.

The term "hybridizable under high stringency conditions" referred to herein means capable of specific binding under conditions whereby only nucleic acid sequences having a substantial identity of greater than 95% with respect to each other will hybridize. These conditions are known in the art and discussed herein.

The term "degenerate codon" means any of the nucleotide codon triplets encoding a desired amino acid according to the genetic code. Codons can be selected based upon known preferred codon usage in a host organism such as *E. coli*.

The term "polypeptide fragment" as used herein refers to a polypeptide that has an amino-terminal and/or carboxy-terminal deletion, but where the remaining amino acid sequence is identical to the corresponding positions in the naturally-occurring sequence deduced, for example, from a full-length DNA sequence. Fragments typically are at least 3 amino acids long, preferably are 5-10 amino acids long, more preferably are 10-50 amino acids long, even more preferably are more than 50 amino acids long and comprise at least one extracellular domain of a GBS toxin receptor. Most preferred are fragments that comprise the entire extracellular domains of a GBS toxin receptor, and preferably also comprise portions of transmembrane and intracellular domains sufficient to maintain the polypeptide fragment in a functional stereochemical conformation on the surface of a cell, lipid membrane, liposome, micelle, or other lipophilic structure.

The term "immunologically reactive" means having antigenic properties or being capable of

being specifically bound by an antibody that can specifically bind GBS toxin receptor. A substance has antigenic properties if it can generate monoclonal or polyclonal antibodies when administered to an animal under conditions known in the art to facilitate the production of antibodies that will recognize and bind a particular antigen.

A "heterologous polypeptide" is a polypeptide different from polypeptides normally produced by a particular cell. For example, a GBS toxin receptor polypeptide or fragment thereof that is produced recombinantly in a cell that does not normally produce such GBS toxin receptor polypeptide or fragment thereof, is a heterologous polypeptide. A second polypeptide joined to a GBS toxin receptor polypeptide or fragment thereof is also a heterologous polypeptide if it is not joined to a GBS toxin receptor polypeptide in nature.

As used herein, the terms "label" or "labeled" refers to incorporation of a detectable marker, e.g., by incorporation of a radiolabeled amino acid or attachment to a polypeptide of biotinyl moieties that can be detected by marked avidin (e.g., streptavidin containing a fluorescent marker or enzymatic activity that can be detected by optical or colorimetric methods). Various methods of labeling polypeptides and glycoproteins are known in the art and may be used. Examples of labels for polypeptides include, but are not limited to, the following: radioisotopes (e.g., ^{3}H, ^{14}C, ^{35}S, ^{125}I, ^{131}I), fluorescent labels (e.g., FITC, rhodamine, lanthanide phosphors), enzymatic labels (e.g., horseradish peroxidase, ß-galactosidase, luciferase, alkaline phosphatase), chemiluminescent, biotinyl groups, predetermined polypeptide epitopes recognized by a secondary reporter (e.g., leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags). In some embodiments, labels are attached by spacer arms of various lengths to reduce potential steric hindrance.

The term "compound" as used herein preferably refers to a peptidic, peptidomimetic, organic, or other chemical molecule and also refers to a nucleic acid molecule or chemical derivative thereof. The compound can interact with, or be, the polynucleotides or polypeptides of the invention.

The singular forms "a", "an" and "the" include plural referents unless the context clearly dictates otherwise.

The SEQ ID NOs of the nucleic acid and amino acid sequences described herein are summarized below in Table 1.

Table 1
Nucleic Acid and Amino Acid Sequences

SEQ ID NO:	Type of Sequence	Description
SEQ ID NO: 1	nucleic acid	Partial human GBS toxin receptor (HP55)
SEQ ID NO: 2	amino acid	Partial human GBS toxin receptor (HP55)
SEQ ID NO: 3	nucleic acid	Sheep GBS toxin receptor (SP55)
SEQ ID NO: 4	amino acid	Sheep GBS toxin receptor (SP55)
SEQ ID NO: 5	nucleic acid	Primer
SEQ ID NO: 6	nucleic acid	Primer
SEQ ID NO: 7	nucleic acid	Full-length human GBS toxin receptor (HP59)
SEQ ID NO: 8	amino acid	Full-length human GBS toxin receptor (HP59)
SEQ ID NO: 9	nucleic acid	Human/Sheep consensus GBS toxin receptor coding region (with base codes a, c, g, t, m, r, w, s, y, k)
SEQ ID NO: 10	amino acid	Human/Sheep consensus GBS toxin receptor coding region (translation of SEQ ID No: 9)
SEQ ID NO: 11	nucleic acid	Human/Sheep consensus GBS toxin receptor coding region (with base codes a, c, g, t, n)
SEQ ID NO: 12	amino acid	Human/sheep consensus GBS toxin receptor coding region (translation of SEQ ID NO: 11)

The headings provided herein describe the general topic discussed and are not intended to be exclusive of information discussed in other sections. Frequently, information, methods, compositions, and other aspects may be applicable to more than one embodiment of the invention and can be so combined.

INTRODUCTION

GBS toxin binds to tissues undergoing pathologic, hypoxia-driven, and embryologic angiogenesis or neovascularization. The inventors have identified at least two mammalian GBS toxin receptors, which are described herein. Examples 1 and 2 describe the cloning and characterization of some GBS toxin receptors. The inventors have classified GBS toxin receptor as an integral protein with seven transmembrane domains. The predicted segments are shown in Table 7. The protein has several putative sites for phosphorylation by cAMP-dependent kinase, protein kinase C (PKC), and casein kinase II (CK2). Typically, such integral proteins, upon binding of a molecule (e.g., a ligand or an extracellular messenger), undergo a conformational change which facilitates phosphorylation at phosphorylation sites such as those discussed above. The phosphorylation of the protein at these sites may trigger a signal transduction cascade, which often results in proliferation or other nuclear responses of the cells which have been exposed to the binding molecule. Angiogenesis or neovascularization involves proliferation and migration of endothelial cells. As discussed in greater detail in Examples 4 and 5, GBS toxin

receptor expression is correlated with medical conditions involving pathologic, hypoxia-driven, and embryogenic angiogenesis or neovascularization. GBS toxin receptor polypeptides can be used for a variety of purposes, including screening for compounds that can inhibit endothelial cell proliferation and/or migration mediated by GBS toxin receptor and screening for cytotoxic chimeric compounds that can bind to and destroy cells expressing GBS toxin receptor. GBS toxin receptor polynucleotides can be used for a variety of purposes, including the design of antisense polynucleotides that can block translation of messenger RNA encoding GBS toxin receptor.

POLYNUCLEOTIDES

One aspect of the invention provides for isolated polynucleotides at least ten bases in length encoding or complementary to a nucleic acid sequence encoding a GBS toxin receptor or a fragment derived therefrom. Preferably, the GBS toxin receptor is a mammalian GBS toxin receptor, more preferably an ovine, bovine or feline GBS toxin receptor, and most preferably a human GBS toxin receptor. The isolated polynucleotides can be naturally occurring or non-naturally occurring. The isolated polynucleotides can comprise a DNA sequence or an RNA sequence in which every T is replaced with U. For purposes of determining percentage identity, T is considered equivalent to U. Preferably, the polynucleotides include alleles of an ovine, bovine, feline or human GBS toxin receptor, and can include alleles of GBS toxin receptor of other mammals. These polynucleotides can be isolated using polynucleotides derived from SEQ ID NOs: 1, 3, 7, 9 and 11, as described further below.

Polynucleotides, oligonucleotides and fragments of the invention selectively hybridize to nucleic acid strands under hybridization and wash conditions that minimize appreciable amounts of detectable binding to nonspecific nucleic acids. The polynucleotides can be hybridizable under high stringency conditions to a nucleic acid molecule having a nucleic acid sequence comprising at least 20 contiguous polynucleotides, preferably at least 30 contiguous nucleotides of SEQ ID NO: 1 or SEQ ID NO: 3, and even more prefereably to the nucleic acid sequence of SEQ ID NO: 1, 3, 7, 9 or 11 or the complement of SEQ ID NO: 1, 3, 7, 9 or 11. Such polynucleotides can be used for performing selective, high stringency hybridization and are particularly useful for performing amplification of nucleic acid by polymerase chain reaction (PCR) to determine the presence or absence of GBS toxin receptor in a sample, for isolating a naturally occurring nucleic acid encoding a GBS toxin receptor (see Example 3), as antisense molecules for blocking translation of GBS toxin receptor mRNA. Particularly preferred are polynucleotides hybridizable under high stringency conditions to a nucleic acid molecule having a nucleic acid sequence comprising the nucleic acid sequence of nucleotides 266 to 1870 of SEQ ID NO: 7 (the putative full length coding region of a human GBS toxin receptor, excluding the start codon),

nucleotides 266 to 1870 of SEQ ID NO:7 (the putative full length coding region of a human GBS toxin receptor, including the start codon), nucleotides 61 to 1542 of SEQ ID NO:1 (the partial coding region of a human GBS toxin receptor, excluding the start codon), nucleotides 58 to 1542 of SEQ ID NO: 1 (the partial coding region of a human GBS toxin receptor, including the start codon), nucleotides 87 to 1568 of SEQ ID NO: 3 (the coding region of a sheep GBS toxin receptor, excluding the start codon), nucleotides 84 to 1568 of SEQ ID NO:3 (the coding region of a sheep GBS toxin receptor, including the start codon), or a complementary nucleic acid sequence thereof.

The polynucleotides can have an identity to the nucleic acid sequence of a corresponding region of SEQ ID NO: 1, 3 or 7 or the complement of a corresponding region of SEQ ID NO: 1, 3 or 7 in the range of about 85% to 100%, preferably greater than about 87% identity, more preferably greater than about 95% identity, and most preferably about 99% to 100% identity. Particularly preferred are polynucleotides comprising the nucleic acid sequence of nucleotides 266 to 1870 of SEQ ID NO: 7, or nucleotides 87 to 1568 of SEQ ID NO: 3, SEQ ID NO: 9, SEQ ID NO:11, or a complementary nucleic acid sequence thereof.

Preferably, the polynucleotides comprise a nucleic acid sequence encoding, or complementary to a nucleic acid sequence encoding, a polypeptide having an identity to the amino acid sequence of a fragment of a GBS toxin receptor in the range of about 85% to 100%, more preferably greater than 86% identity, even more preferably greater than 95% identity, and most preferably 99% to 100% identity. Preferably, the fragment binds GBS toxin. Preferred fragments comprise all or a portion of residues 1 to 495 of SEQ ID NO: 2 or all or a portion of residues 1 to 536 of SEQ ID NO: 8. Particularly preferred are polynucleotides comprising a nucleic acid sequence encoding a polypeptide having 100% identity to the amino acid sequence of residues 1 to 495 of SEQ ID NO: 4, residues 1 to 495 of SEQ ID NO: 2, or residues 1 to 536 of SEQ ID NO:8.

Polynucleotides encoding naturally occurring GBS toxin receptor can be isolated from various tissue sources and cell cultures from different species that produce such a receptor by the methods described herein, such as, for example, cells from tumor endothelium, synovial tissue in rheumatoid arthritis, or hypoxic tissue deprived of or restricted from blood flow, such as in reperfusion injury or wounded tissue. Such polynucleotides can be isolated by hybridization using probes or by polymerase chain reaction using oligonucleotides, as well as by implementing other molecular biology techniques known in the art. Such probes and oligonucleotides typically comprise various regions of the sequence of SEQ ID NO: 1, 3, 7, 9 or 11, preferably of SEQ ID NO: 1, 3, or 7, or encode various regions of the sequence of SEQ ID NO. 2, 4, 8,10 or 12, preferably of SEQ NO: 2, 4 or 8.

Polynucleotides useful for cloning genes encoding GBS toxin receptors of various organisms can

be determined by comparing the amino acid sequences of homologous proteins. (see Table 4). For example, conserved regions can be targeted for the synthesis of oligonucleotides or degenerate oligonucleotides to be used as probes for hybridization or nucleic acid amplification, techniques discussed further below and in Example 3. Stringency can be varied to achieve selective hybridization conditions whereby nucleic acid sequences having less than 95% identity with respect to each other will hybridize. These conditions are known in the art and discussed herein and examples are provided. Generally, the nucleic acid sequence identity between the polynucleotides, oligonucleotides, and fragments of the invention and a nucleic acid sequence of interest will be at least about 85%, and more typically with preferably increasing identities of at least about 90%, 95%, 99%, and 100%.

Polynucleotides can be used as probes under high stringency wash conditions and with corresponding hybridization conditions, as known in the art. Small polynucleotides, for example, polynucleotides 200 bases or fewer in length, are often referred to in the art as oligonucleotides. Techniques for using polynucleotides as probes to detect the same or related nucleic acid sequences is well known in the art. See, for example, Sambrook et al, especially Chapter 11, the text of which is herein incorporated by reference. Usually, probes can be made from polynucleotides that are 10 to 200 bases in length. Preferably probes are made from polynucleotides 10 to 60 nucleotides in length and most preferably 12 to 40 bases in length. Specific probes can be designed based on results obtained using nucleic acid homology computer programs such as FASTA, which uses the method of Pearson and Lipman (*Proc. Natl. Acad. Sci. USA* 85:2444-2448 (1988)) and shows the degree of identity between compared sequences. The size of the probe is dependent upon the region of the gene to which it will be hybridized. The size of the probe increases as the degree of homology to undesirable nucleic acid sequences increases. A probe 10-50 nucleotides in length can be used, preferably more than 50 nucleotides, even more preferably more than 100 nucleotides, and most preferably a probe made from the entire coding region of a GBS toxin receptor will be used. To decrease the number of false positives, preferably two probes are used to identify clones that bind to both probes under hybridization and wash conditions. Oligonucleotides can be synthesized on an Applied BioSystems oligonucleotide synthesizer according to specifications provided by the manufacturer.

Typically, hybridization and washing conditions are performed at according to conventional hybridization procedures. Typical hybridization conditions for screening plaque lifts (Benton and Davis (1978) *Science* 196: 180) can be: 50% formamide, 5 x SSC (sodium chloride, sodium citrate) or SSPE (sodium chloride, sodium phosphate, EDTA), 1-5 x Denhardt's solution, 0.1-1% SDS, 100-200 μg sheared heterologous DNA or tRNA, 0-10% dextran sulfate, 1×10^5 to 1×10^7 cpm/ml of denatured probe with a specific activity of about 1×10^8 cpm/μg, and incubation at 42°C for about 6-36 hours.

Prehybridization conditions are essentially identical except that probe is not included and incubation time is typically reduced. Washing conditions are typically 1-3 x SSC, 0.1-1% SDS, 42-70°C with change of wash solution at about 5-30 minutes. Cognate bacterial sequences, including allelic sequences, can be obtained in this manner. For high stringency hybridization conditions, various parameters can be altered to increase the stringency of hybridization, such as by increasing the temperature of incubation with the labeled probe. Preferably, for greater flexibility in experimental design, the probe can be hybridized at a lower temperature, such as, for example, room temperature and the stringency can then be modified by altering the salt concentration and temperature of the wash solutions. For high stringency a wash temperature of greater than or equal to 42°C can be used, such as, for example, 68°C, in a wash buffer having a salt concentration less than 3X SSC, such as, for example, 0.1X SSC. In some cases, TMACL can also be used, particularly for polynucleotides rich in G-C base pairs in order to decrease non-specific binding. A lower stringency wash can be used to hybridize polynucleotides with lower identities or polynucleotides that are less than 60 base pairs in length. For a low stringency wash, temperatures of less than or equal to 42° can be used in a wash buffer having a salt concentration of greater than or equal to 2X SSC.

The invention includes methods for amplification of target nucleic acids, such as the polymerase chain reaction ("PCR") technique. The PCR technique can be applied to identify related sequences in the genomes of various organisms and to detect nucleotide sequences in suspected samples, using oligonucleotide primers spaced apart from each other and based on the genetic sequence set forth herein. The primers are complementary to opposite strands of a double-stranded DNA molecule and are typically separated by from about 50 to 450 nucleotides or more (usually not more than 2000 nucleotides). This method entails preparing the specific oligonucleotide primers followed by repeated cycles of target DNA denaturation, primer binding, and extension with a DNA polymerase to obtain DNA fragments of the expected length based on the primer spacing. Extension products generated from one primer serve as additional target sequences for the other primer. The degree of amplification of a target sequence is controlled by the number of cycles that are performed and is theoretically calculated by the simple formula 2n where n is the number of cycles. Given that the average efficiency per cycle ranges from about 65% to 85%, 25 cycles produce from 0.3 to 4.8 million copies of the target sequence. The PCR method is described in a number of publications, including Saiki et al., *Science* (1985) 230:1350-1354; Saiki et al., *Nature* (1986) 324:163-166; and Scharf et al., *Science* (1986) 233:1076-1078. Also see U.S. Patent Nos. 4,683,194; 4,683,195; and 4,683,202, the text of each patent is herein incorporated by reference. Additional methods for PCR amplification are described in: PCR Technology: Principles and Applications for DNA Amplification ed. HA Erlich, Freeman Press, New

York, NY (1992); *PCR Protocols: A Guide to Methods and Applications*, eds. Innis, Gelfland, Snisky, and White, Academic Press, San Diego, CA (1990); Mattila et al. (1991) *Nucleic Acids Res.* 19: 4967; Eckert, K.A. and Kunkel, T.A. (1991) *PCR Methods and Applications 1*: 17, and; *PCR*, eds. McPherson, Quirkes, and Taylor, IRL Press, Oxford, all of which are incorporated herein by reference.

In yet another embodiment, an antisense polynucleotide can be administered to a mammal to treat or prevent a medical condition involving pathologic and/or hypoxia-driven angiogenesis. The antisense oligonucleotides of the invention can be synthesized by any of the known chemical oligonucleotide synthesis methods. Such methods are generally described, for example, in Winnacker, From Genes to Clones: Introduction to Gene Technology. VCH Verlagsgesellschaft mbH (H., Ibelgaufts trans. 1987). Any of the known methods of oligonucleotide synthesis can be utilized in preparing the instant antisense oligonucleotides. The antisense oligonucleotides are most advantageously prepared by utilizing any of the commercially available, automated nucleic acid synthesizers. The device utilized to prepare the oligonucleotides described herein, the Applied Biosystems 380B DNA Synthesizer, utilizes - cyanoethyl phosphoramidite chemistry. Antisense oligonucleotides hybridizable with any portion of the mRNA transcript can be prepared by the oligonucleotide synthesis methods known to those skilled in the art. While any length oligonucleotide can be utilized in the practice of the invention, sequences shorter than 12 bases may be less specific in hybridizing to the target GBS toxin receptor mRNA, and may be more easily destroyed by enzymatic digestion. Hence, oligonucleotides having 12 or more nucleotides are preferred. Sequences longer than 18 to 21 nucleotides may be somewhat less effective in inhibiting GBS toxin receptor translation because of decreased uptake by the target cell. Thus, oligomers of 12-21 nucleotides are most preferred in the practice of the present invention, particularly oligomers of 12-18 nucleotides. Oligonucleotides complementary to and hybridizable with any portion of the GBS toxin receptor mRNA transcript are, in principle, effective for inhibiting translation of the transcript, and capable of inducing the effects herein described. Translation is most effectively inhibited by blocking the mRNA at a site at or near the initiation codon. Thus, oligonucleotides complementary to the 5' region of the GBS toxin receptor mRNA transcript are preferred. Secondary or tertiary structure which might interfere with hybridization is minimal in this region. Moreover, sequences that are too distant in the 3' direction from the initiation site can be less effective in hybridizing the mRNA transcripts because of a "read-through" phenomenon whereby the ribosome is postulated to unravel the antisense/sense duplex to permit translation of the message. (see, e.g. Shakin, J. Biochemistry 261, 16018 (1986)). The antisense oligonucleotide is preferably directed to a site at or near the ATG initiation codon for protein synthesis. Oligonucleotides complementary to a portion of the GBS toxin receptor mRNA including the initiation codon are preferred. While antisense oligomers complementary to the 5' region of the GBS

toxin receptor transcript are preferred, particularly the region including the initiation codon, it should be appreciated that useful antisense oligomers are not limited to those complementary to the sequences found in the translated portion of the mRNA transcript, but also includes oligomers complementary to nucleotide sequences contained in, or extending into, the 5' and 3' untranslated regions. Antisense nucleotides or antisense expression constructs can find use to treat or prevent diseases associated with pathologic or hypoxia-driven angiogenesis and neovascularization, as inappropriate expression of GBS toxin receptor results in hyperproliferation of endothelial cells.

In one embodiment, the polynucleotides of the invention can exist in linear form. In another embodiment, the polynucleotides can exist in circular form as part of a plasmid.

In yet another embodiment, a probe or PCR primer comprises a group of polynucleotide species containing different degenerate codons at various positions, which polynucleotides encode, or are complementary to sequences encoding, a GBS toxin receptor in whole or in part. Such polynucleotides can be useful for isolating nucleic acid sequences encoding polypeptides having at least about 85% identity to the amino acid sequence of sheep or human GBS toxin receptor, such as, for example, GBS toxin receptors of other organisms. Typically, such polynucleotides are synthesized chemically as described above by programming a synthesizer to incorporate a particular combination of nucleic acid residues at a certain position. Typical designations are shown in Table 2.

Table 2

Base Codes

Symbol	Meaning
A	A; adenine
C	C; cytosine
G	G; guanine
T	T; thymine
U	U; uracil
M	A or C
R	A or G
W	A or T/U
S	C or G
Y	C or T/U
K	G or T/U
V	A or C or G; not T/U
H	A or C or T/U; not G
D	A or G or T/U; not C
B	C or G or T/U; not A
N	A or C or G or T/U

POLYPEPTIDES

Another aspect of the invention provides polypeptides comprising (1) the full length GBS toxin receptor protein or a naturally occurring allelic variant thereof, (2) fragments of at least 3 amino acids of the amino acid sequence of SEQ ID NO: 2, 4, 8, 10 or 12, and (3) a GBS toxin receptor protein, polypeptide, or polypeptide fragment having an amino acid identity in the range of about 80% to 100% to the amino acid sequence of a corresponding region of SEQ ID NO: 2, 4 or 8. Preferred fragments of the amino acid sequence of SEQ ID NO: 2, 4, 8, 10 or 12, are at least 5, 6, 7, 8 or 9 amino acids in length and are immunologically reactive, i.e., immunogenic. More preferred are fragments at least 25 amino acids in length and fragments comprising the amino acid sequence of residues 181 to 419 of SEQ ID NO: 2 or residues 1 to 240 of SEQ ID NO: 4. Most preferred are fragments that can bind GBS toxin. Preferably, the GBS toxin receptor protein, polypeptide, or polypeptide fragment has an amino acid identity to the amino acid sequence of a corresponding region of SEQ ID NO: 2, 4 or 8 of at least about 86%, more preferably at least about 95% identity, even more preferably at least about 99% identity up to having one amino acid difference, and most preferably 100% identity. Preferred polypeptides have at least about 89% identity, more preferably at least about 95% identity, even more preferably at least about 99% identity up to having one amino acid difference, and most preferably 100% identity to the amino acid sequence of residues 181 to 419 of SEQ ID NO: 2, residues 1 to 495 of SEQ ID NO: 4. Preferably, a full length GBS toxin receptor protein comprises the amino acid sequence of residues 1 to 495 of SEQ ID NO: 2, residues 1 to 495 of SEQ ID NO: 4, or residues 1 to 536 of SEQ ID NO: 8, or an allelic variant thereof. The polypeptides of the invention can include amino acids in addition to the GBS toxin receptor protein, polypeptide, or polypeptide fragment. Such polypeptides typically comprise a heterologous polypeptide joined to a second polypeptide derived, as described above, from a GBS toxin receptor. Preferably the additional amino acids are covalently linked to the amino-terminal or carboxy-terminal terminus of the GBS toxin receptor protein, polypeptide, or polypeptide fragment.

Fragments or analogs of GBS toxin receptor can be prepared by those of ordinary skill in the art. Preferred amino- and carboxy-termini of fragments or analogs occur near boundaries of functional domains. For example, such functional domains include domains conferring the property of induction of an inflammatory response upon binding of GBS toxin to the GBS toxin receptor. GBS toxin mediates the binding and opsonization by C3 of endothelial cells that express the GBS toxin receptor. Such domains can comprise the binding site for GBS toxin, in whole or in part, or domains otherwise essential for GBS toxin receptor structure and/or function. Preferably, computerized comparison methods are used to identify sequence motifs or predicted protein conformation domains that occur in other proteins of known structure and/or function. Methods to identify protein sequences that fold into a known three-

dimensional structure are known (Bowie et al. (1991) *Science* 253: 164). Computerized prediction methods, such as, for example, a hydropathy profile as provided by the "Soap" program in PC/GENE can be employed to identify putative structural and functional domains. Using the method of Klein, Kanehisa and DeLise, Biochim Biophys Acta (1985) 815:468-476, the inventors have classified a sheep GBS toxin receptor, SP55, as an integral protein with seven transmembrane segments predicted. Such a protein is also known colloquially in the art as a "7-spanner". The predicted segments are set forth below in Table 3.

Table 3

Predicted Transmembrane Domains of SP55

	Inner Boundaries		Outer Boundaries		Segment	P:I odds*
No.	From	To	From	To	Sequence	
1	232	248	226	252	FFGIVGIIWFILWICLV (232-248 of SEQ ID No. 4)	2.589323E-05
2	369	385	365	389	LIGMIGPAIFLVAAGFI (369-385 of SEQ ID No. 4)	1.007311E-03
3	458	474	456	479	TVFCIAAAINVFGAIFF (458-474 of SEQ ID No. 4)	2.482542E-03
4	137	153	135	157	LLLGFGIFATAIFTLFT (137-153 of SEQ ID No. 4)	7.564906E-03
5	42	58	42	58	LAFLSFFGFFVLYSLRV (42-58 of SEQ ID No. 4)	8.236557E-02
6	328	344	328	345	GFLSAVPYLGCWLCMIL (328-344 of SEQ ID No. 4)	.1925022
7	390	406	390	407	SLAVAFLTISTTLGGFC (390-406 of SEQ ID No. 4)	.8064944

* Relates hydrophobicity of integral sequence to the hydrophobicity of the peripheral sequence. An integral sequence with a higher hydrophobicity number is more likely to be part of a transmembrane domain.

A computerized alignment of the amino acid sequences of GBS toxin receptor in various organisms provides further guidance in preparing preferred fragments. See, for example, Table 4 which compares the amino acid sequence of residues 42 to 536 of a human GBS toxin receptor (HP59) (residues 42 to 536 of SEQ ID NO: 8) and a sheep GBS toxin receptor (SP55).

Table 4

Alignment of Human and Sheep GBS Toxin Receptor Amino Acid Sequences

```
SP55    MKSPVSDLAPSDGEEGSDRTPLLQRAPRAEPAPVCCSARYNLAFLSFFGF     50
        | ||| |||  ||||  ||||||  ||||| |||||||||||| | ||||
HP55    MRSPVRDLARNDGEESTDRTPLLPGAPRAEAAPVCCSARYNLAILAFFGF     50

SP55    FVLYSLRVNLSVALVDMVDSNTTAKDNRTSYECAEHSAPIKVLHNQTGKK    100
        |  | ||||||||||||||||||  |||||  | |||||||| |||||||
HP55    FIVYALRVNLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVHHNQTGKK    100

SP55    YRWDAETQGWILGSFFYGYIITQIPGGYVASRSGGKLLLGFGIFATAIFT    150
        | |||||||||||||||||||||||||||||  ||| ||||||  ||  |
HP55    YQWDAETQGWILGSFFYGYIITQIPGGYVASKIGGKMLLGFGILGTAVLT    150

SP55    LFTPLAADFGVGALVALRALEGLGEGVTYPAMHAMWSSWAPPLERSKLLS    200
        |||| ||| ||| |  |||||||||||| |||||||||||||||||||||
HP55    LFTPIAADLGVGPLIVLRALEGLGEGVTFPAMHAMWSSWAPPLERSKLLS    200

SP55    ISYAGAQLGTVVSLPLSGVICYYMNWTYVFYFFGIVGIIWFILWICLVSD    250
        ||||||||||| |||||| |||||||||||||||  || || ||| ||||
HP55    ISYAGAQLGTVISLPLSGIICYYMNWTYVFYFFGTIGIFWFLLWIWLVSD    250

SP55    TPETHKTITPYEKEYILSSLKNQLSSQKSVPWIPMLKSLPLWAIVVAHFS    300
        ||  || |  |||||||||| ||||||||||| | |||||||||||||||
HP55    TPQKHKRISHYEKEYILSSLRNQLSSQKSVPWVPILKSLPLWAIVVAHFS    300

SP55    YNWTFYTLLTLLPTYMKEVLRFNIQENGFLSAVPYLGCWLCMILSGQAAD    350
        |||||||||||||||||| |||| |||||||  |||| ||||||||||||
HP55    YNWTFYTLLTLLPTYMKEILRFNVQENGFLSSLPYLGSWLCMILSGQAAD    350

SP55    NLRARWNFSTLWVRRVFSLIGMIGPAIFLVAAGFIGCDYSLAVAFLTIST    400
        |||| |||||| ||| |||||||||| |||||||||||||||||||||||
HP55    NLRAKWNFSTLCVRRIFSLIGMIGPAVFLVAAGFIGCDYSLAVAFLTIST    400

SP55    TLGGFCSSGFSINHLDIAPSYAGILLGITNTFATIPGMIGPIIARSLTPE    450
        |||||||||||||||||||||||||||||||||||||| || || ||||
HP55    TLGGFCSSGFSINHLDIAPSYAGILLGITNTFATIPGMVGPVIAKSLTPD    450

SP55    NTIGEWQTVFCIAAAINVFGAIFFTLFAKGEVQNWAISDHQGHRN         495
        || ||||||| |||||||||||||||||||||||||  || |||
HP55    NTVGEWQTVFYIAAAINVFGAIFFTLFAKGEVQNWALNDHHGHRH         495
```

HP55 - SEQ ID NO: 2
SP55 - SEQ ID NO: 4

Thus, the foregoing examples demonstrate that those of skill in the art can recognize sequence motifs and structural conformations that may be used to define structural and functional domains in a GBS toxin receptor sequence.

Although one class of preferred embodiments are fragments having amino- and/or carboxy-termini corresponding to amino acid positions near functional domains borders, alternative fragments may be prepared. The choice of the amino- and carboxy-termini of such fragments rests with the

discretion of the practitioner and will be made based on experimental considerations, such as ease of construction, stability to proteolysis, thermal stability, immunological reactivity, amino- or carboxyl-terminal residue modification, or other considerations. Polypeptide fragments usually contain at least nine amino acids and can contain any number of amino acids provided that the peptide fragment is at least about 80% identical to the corresponding fragment of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO:8. The human GBS toxin receptor has 41 additional amino acids on the N-terminus compared to the sheep GBS toxin receptor (compare SEQ ID NO:4 and SEQ ID NO:8). Analogs can comprise additions or deletions of some or all of those 41 N-terminal amino acids. N-terminal and C-terminal additions useful, e.g., for purification and/or antibody recognition are also contemplated. Examples include histidine tags, a FLAG (phenylalanine, leucine, alanine, guanine) epitope, fusion partners such as glutathione S transferase, chloramphenicol acetyltransferase (CAT), luciferase, β-galactosidase, and the like. Deletions of unconserved amino acids are also contemplated, provided that the structural integrity and/or binding properties of the GBS toxin receptor are not substantially compromised.

Analogs can also comprise amino acid substitutions, preferably conservative substitutions. Also preferred are conservative and/or non-conservative substitutions in regions having less shared identity among various species. For example, a variant of a GBS toxin receptor can comprise conservative and/or non-conservative substitutions of amino acids corresponding to residues 2, 6, 10, 11, 16, 17, 24, 31, 44, 46, 52, 53, 55, 74, 75, 81, 82, 84, 93, 102, 132, 133, 137, 144, 145, 148, 149, 155, 159, 163, 165, 166, 179, 212, 219, 235, 236, 239, 242, 246, 253, 254, 257, 259, 260, 271, 283, 285, 319, 324, 332, 333, 338, 355, 362, 366, 377, 439, 442, 445, 450, 453, 461, 487, 488, 491 and 495 of SEQ ID NO:4. Preferably the substitution is an amino acid present in the corresponding position of SEQ ID NO:4 or SEQ ID NO:8. For example, referring to the alignment plot in Table 4, the amino acid corresponding to position 152 of SEQ ID NO:4 can be arginine (R), glutamine (Q), or a conservative or non-conservative substitution of R or Q, and preferably is R or Q. Such regions can be identified by amino acid sequence alignment plots, such as that shown in Table 4. Preferred amino acid substitutions are those which: (1) reduce susceptibility to proteolysis, (2) reduce susceptibility to oxidation, (3) alter binding affinity for GBS toxin, and (4) confer or modify other physicochemical or functional properties of such analogs. Analogs can include various mutations of a sequence other than the naturally-occurring peptide sequence, such as, for example, single or multiple amino acid substitutions.

A conservative amino acid substitution should generally not substantially change the structural characteristics of the parent sequence (e.g., a replacement amino acid should not tend to break a helix that occurs in the parent sequence, disrupt disulfide bonds or disrupt other types of secondary structure that characterizes the parent sequence). Examples of art-recognized polypeptide secondary and tertiary

structures are described in *Proteins, Structures and Molecular Principles*, (1984) Creighton (ed.), W.H. Freeman and Company, New York; *Introduction to Protein Structure*, (1991), C. Branden and J. Tooze, Garland Publishing, New York, NY; and Thornton et al. (1991) *Nature* 354: 105 (which are incorporated herein by reference). A conservative substitution is a "replacement of an amino acid in a polypeptide by one with similar characteristics." (McGraw-Hill Dictionary of Scientific and Technical Terms, Fifth Edition, 1994, Sybil P. Parker, Editor in Chief). The structure and characteristics of naturally occurring amino acids has long been known in the art (Biochemistry, Second Edition, Albert L. Lehninger, 1975, pages 71-76) For example, amino acids which are similar by virtue of their hydrophobic R groups are alanine, valine, leucine, isoleucine, proline, phenylalanine, tryptophan, and methionine. Alanine, valine, leucine, and isoleucine are similar by virtue of their aliphatic R groups. Phenylalanine and tryptophan are similar by virtue of their aromatic R groups. Glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine are similar by virtue of their uncharged polar R groups. Glycine and alanine are similar by virtue of their small size. Serine and threonine are similar by virtue of a hydroxyl in their R group. Asparagine and glutamine differ by only one methyl group. Similarly, aspartic acid and glutamic acid differ by only one methyl group, and they are similar by virtue of their acidic R groups. Lysine, arginine, and histidine are similar by virtue of their basic R groups. In addition, lysine and arginine are similar by virtue of the amino groups on the end of the aliphatic chain in their R groups. Tyrosine and phenylalanine are similar by virtue of their aromatic groups. Amino substitutions commonly made in the art include a substitution of valine for leucine or isoleucine, alanine for glycine, serine for threonine, asparagine for glutamine, aspartic acid for glutamic acid, and lysine for arginine, tyrosine for phenylalanine, and vice versa.

Typically, one skilled in the art would generally refrain from changing amino acids that are conserved among the various GBS toxin receptors, but a conservative substitution might reasonably be made. For example, Table 4 guides one skilled in the art to avoid substitutions, particularly nonconservative substitutions, for amino acids corresponding to residues 1, 3-5, 7-9, 12-15, 18-23, 26-30, 32-43, 45, 47-51, 54, 56-73, 76-80, 83, 85-92, 94-101, 103-131, 134-136, 138-143, 146-147, 150-154, 156-158, 160-162, 164, 167-178, 180-211, 213-218, 220-234, 237-238, 240-241, 243-245, 247-252, 255-256, 258, 261-270, 272-282, 284, 286-318, 320-323, 325-331, 334-337, 339-354, 356-361, 363-365, 367-376, 378-438, 440-441, 443-444, 446-449, 451-452, 454-460, 462-486, 489-490 and 492-494 of SEQ ID NO:4, which are conserved among the GBS toxin receptors shown in Table 4.

Tables 5 and 6 describe sequences within HP59 and SP55, respectively, that match predicted amidation, N-glycosylation, cAMP-phosphorylation, CK2-phosphosylation, myristylation (addition of unsaturated fatty acid molecules), and PKC-phosphosylation sites (Omega 1.1 sequence analysis

program). The information contained in these tables provides guidance to one skilled in the art for designing GBS toxin receptor variants and fragments. When designing polypeptide variants, for example, one may decide to avoid substitutions in some or all of these regions. When designing polypeptide fragments other than immunogenic polypeptide fragments, for example, one may opt to include some or all of these regions.

Table 5
Putative Recognition Sites in HP59

Site	Seq. ID NO: 8 Residues:	Sequence
AMIDATION	23-26	SGRR
AMIDATION	138-141	TGKK
ASN_GLYCOSYLATION	100-103	NLSV
ASN_GLYCOSYLATION	112-115	NTTL
ASN_GLYCOSYLATION	118-121	NRTS
ASN_GLYCOSYLATION	136-139	NQTG
ASN_GLYCOSYLATION	266-269	NWTY
ASN_GLYCOSYLATION	343-346	NWTF
ASN_GLYCOSYLATION	398-401	NFST
CAMP_PHOSPHO_SITE	297-300	KRIS
CK2_PHOSPHO_SITE	113-116	TTLE
CK2_PHOSPHO_SITE	114-117	TLED
CK2_PHOSPHO_SITE	300-303	SHYE
CK2_PHOSPHO_SITE	493-496	TVGE
MYRISTYL	66-71	GAPRAE
MYRISTYL	167-172	GGYVAS
MYRISTYL	183-188	GILGTA
MYRISTYL	213-218	GLGEGV
MYRISTYL	246-251	GAQLGT
MYRISTYL	250-255	GTVISL
MYRISTYL	378-383	GSWLCM
MYRISTYL	427-432	GCDYSL
MYRISTYL	444-449	GGFCSS
MYRISTYL	464-469	GILLGI
MYRISTYL	468-473	GITNTF
PKC_PHOSPHO_SITE	23-25	SGR
PKC_PHOSPHO_SITE	58-60	TDR
PKC_PHOSPHO_SITE	78-80	SAR
PKC_PHOSPHO_SITE	120-122	TSK
PKC_PHOSPHO_SITE	138-140	TGK
PKC_PHOSPHO_SITE	310-312	SLR
PKC_PHOSPHO_SITE	317-320	SQK

Table 6
Putative Recognition Sites in SP55

Site	Seq. ID NO: 4 Residues:	Sequence
AMIDATION	97-100	TGKK
ASN_GLYCOSYLATION	59-62	NLSV
ASN_GLYCOSYLATION	71-74	NTTA
ASN_GLYCOSYLATION	77-80	NRTS
ASN_GLYCOSYLATION	95-98	NQTG
ASN_GLYCOSYLATION	225-228	NWTY
ASN_GLYCOSYLATION	302-305	NWTF
ASN_GLYCOSYLATION	357-360	NFST
CK2_PHOSPHO_SITE	11-14	SDGE
CK2_PHOSPHO_SITE	73-76	TAKD
CK2_PHOSPHO_SITE	79-82	TSYE
CK2_PHOSPHO_SITE	259-262	TPYE
CK2_PHOSPHO_SITE	452-455	TIGE
MYRISTYL	126-131	GGYVAS
MYRISTYL	142-147	GIFATA
MYRISTYL	162-167	GALVAL
MYRISTYL	172-177	GLGEGV
MYRISTYL	205-210	GAQLGT
MYRISTYL	209-214	GTVVSL
MYRISTYL	337-342	GCWLCM
MYRISTYL	386-391	GCDYSL
MYRISTYL	403-408	GGFCSS
MYRISTYL	423-428	GILLGI
MYRISTYL	427-432	GITNTF
PKC_PHOSPHO_SITE	17-19	SDR
PKC_PHOSPHO_SITE	37-39	SAR
PKC_PHOSPHO_SITE	55-57	SLR
PKC_PHOSPHO_SITE	73-75	TAK
PKC_PHOSPHO_SITE	97-99	TGK
PKC_PHOSPHO_SITE	254-256	THK
PKC_PHOSPHO_SITE	269-271	SLK
PKC_PHOSPHO_SITE	276-278	SQK

In light of the foregoing, preferred polypeptides comprise an amino acid sequence of the formula:

AA1-AAn-AAm

wherein:

AA1 is absent or is M;

AAn is a contiguous chain of 0 to 100 amino acids, preferably of 0 or 41 amino acids, even more preferably of residues 2-42 of SEQ ID NO:8; and

AAm is a contiguous chain of 494 amino acids comprising AA43 through AA536, wherein:

(1) each of AA43, AA47, AA51, AA52, AA57, AA58, AA65, AA66, AA72, AA85, AA87, AA93, AA94, AA96, AA115, AA116, AA122, AA123, AA125, AA134, AA143, AA173, AA174, AA178, AA185, AA186, AA189, AA190, AA196, AA200,

AA204, AA206, AA207, AA220, AA253, AA260, AA276, AA277, AA280, AA283, AA287, AA294, AA295, AA298, AA300, AA301, AA312, AA324, AA326, AA360, AA365, AA373, AA374, AA379, AA396, AA403, AA407, AA418, AA480, AA483, AA486, AA491, AA494, AA502, AA528, AA529, AA532 and AA536 is an essential amino acid or a modified amino acid and preferably is an amino acid residue corresponding to:

(a) residue 43, 47, 51, 52, 57, 58, 65, 66, 72, 85, 87, 93, 94, 96, 115, 116, 122, 123, 125, 134, 143, 173, 174, 178, 185, 186, 189, 190, 196, 200, 204, 206, 207, 220, 253, 260, 276, 277, 280, 283, 287, 294, 295, 298, 300, 301, 312, 324, 326, 360, 365, 373, 374, 379, 396, 403, 407, 418, 480, 483, 486, 491, 494, 502, 528, 529, 532 and 536, respectively, of SEQ ID NO:8;

(b) residue 2, 6, 10, 11, 16, 17, 24, 25, 31, 44, 46, 52, 53, 55, 74, 75, 81, 82, 84, 93, 102, 132, 133, 137, 144, 145, 148, 149, 155, 159, 163, 165, 166, 179, 212, 219, 235, 236, 239, 242, 246, 253, 254, 257, 259, 260, 271, 283, 285, 319, 324, 332, 333, 338, 355, 362, 366, 377, 439, 442, 445, 450, 453, 461, 487, 488, 491 and 495, respectively of SEQ ID NO:4; or

(c) a conservative substitution thereof;

(2) each of AA44-AA46, AA48-AA50, AA53-AA56, AA59-AA64, AA67-AA71, AA73-AA84, AA86, AA88-AA92, AA95, AA97-AA114, AA117-AA121, AA124, AA126-AA133, AA135-AA142, AA144-AA172, AA175-AA177, AA179-AA184, AA187-AA188, AA191-AA195, AA197-AA199, AA201-AA203, AA205, AA208-AA219, AA221-AA252, AA254-AA259, AA261-AA275, AA278-AA279, AA281-AA282, AA284-AA286, AA288-AA293, AA296-AA297, AA299, AA302-AA311, AA313-AA323, AA325, AA327-AA359, AA361-AA364, AA366-AA372, AA375-AA378, AA380-AA395, AA397-AA402, AA404-AA406, AA408-AA417, AA419-AA478, AA481-AA482, AA484-AA485, AA487-AA490, AA492-AA493, AA495-AA501, AA503-AA527, AA530-AA531 and AA533-AA535 is

(a) residue 44-46, 48-50, 53-56, 59-64, 67-71, 73-84, 86, 88-92, 95, 97-114, 117-121, 124, 126-133, 135-142, 144-172, 175-177, 179-184, 187-188, 191-195, 197-199, 201-203, 205, 208-219, 221-252, 254-259, 261-275, 278-279, 281-282, 284-286, 288-293, 296-297, 299, 302-311, 313-323, 325, 327-359, 361-364, 366-372, 375-378, 380-395, 397-402, 404-406, 408-417, 419-478, 481-482, 484-485, 487-490, 492-493, 495-501, 503-527, 530-531 and 533-535, respectively, of SEQ ID NO:8; or

(b) a conservative substitutions thereof; and

(3) AA315 through AA367 are optionally absent.

Preferred polypeptides comprise the amino acid sequence of SEQ ID NO:4, SEQ ID NO:8 or an amino acid sequence which varies from that sequence only at the specific residues which are not conserved between the sheep GBS toxin receptor (SEQ ID NO:4) and the human GBS toxin receptor (SEQ ID NO:8). Of those variations, the most preferred variations are those resulting in a polypeptide encoded by SEQ ID NO:11. Even more preferred variations are those amino acids in the corresponding positions of the amino acid sequence of SEQ ID NO:4. Particularly preferred are polypeptides comprising an amino acid sequence that differs from SEQ ID NO:2, SEQ ID NO:4 or SEQ ID NO:8 at no more than about 20% of the amino acid residues, with increasing preference for no more than about 10%, 5%, 1%, with one to zero amino acid differences being most preferred.

Besides targeting specific amino acids for change, analogs of GBS toxin receptor can also be prepared by techniques involving activity selection, such as, for example, phage display, directed evolution, DNA shuffling, and homologous in procaryotes or eucaryotes of genes from different species, as described in part in U.S. Patent Nos. 5,605,793; 5,830,721; 5,811,238; 5,837,458; 5,093,257; 5,223,409; 5,403,484; 5,571,698; and 5,837,500, which are incorporated herein by reference.

Any variant or fragment of the human and sheep GBS toxin receptors described herein can be tested for the requisite activity by determining whether the variant or fragment can bind GBS toxin.

These polypeptides provide reagents useful in drug discovery and purification and can be used in various *in vitro* assays, preferably when expressed on the surface of a cell, e.g., a stable transfected cell. For example, assays such as binding assays can be used to screen test compounds, including polysaccharides and other compounds, for their ability to bind the GBS toxin receptor. Assays can identify potential drug candidates that block GBS toxin binding to the GBS toxin receptor. Such drugs are useful for preventing and/or treating early onset disease in neonatal humans. Some polypeptides can be used to competitively inhibit binding GBS toxin to a GBS toxin receptor.

The polypeptides of the invention can be used to affinity purify GBS toxin, a GBS toxin chimeric compound, and other polysaccharides or compounds which can bind the GBS toxin receptor.

The polypeptides can also be used to develop a method of targeting a cytotoxic agent for delivery to a cell that expresses a GBS toxin receptor. For example, a cytotoxic agent can be coupled to a molecule that binds a GBS toxin receptor for selective delivery to the neovasculature of a growing tumor. Such a delivery system would permit a highly concentrated, localized attack on a growing tumor, while minimizing the adverse systemic side effects encountered with most chemotherapeutics. In one instance, the cytotoxic agent can be GBS toxin, which, upon binding to GBS toxin receptor, induces an inflammatory response as described in Hellerqvist et al., Angiogenesis: Molecular Biology, Clinical Aspects, Edited by M.E. Maragoudakis et al., Plenum Press, New York 1994, pp. 265-269. In a similar manner, selective delivery of a therapeutic agent to a cell that expresses a GBS toxin receptor could be used advantageously to treat tumors, rheumatoid arthritis or neural injury, or to facilitate wound healing.

The polypeptides of the invention can also be used to screen for and/or design a GBS toxin mimetic with improved therapeutic properties, such as, for example, improved ability to inhibit hypoxia-induced neovascularization or angiogenesis. Such mimetics are useful in the treatment and prevention of conditions resulting from hypoxia-induced neovascularization or angiogenesis, such as, for example, tumor growth, scarring during wound healing, gliosis during repair of neural injury, reperfusion injury, restenosis, rheumatoid arthritis, psoriasis, other chronic inflammatory diseases characterized by angiogenesis, etc. Therapeutic properties can be improved by enhancing biological stability, affinity for

the GBS toxin receptor, complement binding activity, reducing antigenicity, etc.

The polypeptides of the invention can also be used to generate antibodies for various therapeutic and research purposes. The polypeptides of the invention can be used to immunize rabbits, mice, goats, chickens, or other animals known in the art to be amenable to such immunization. Monoclonal antibodies are generally preferred but polyclonal antibodies can also be used, provided that detection of binding of the GBS toxin receptor antibody to the GBS toxin receptor is possible. The production of non-human monoclonal antibodies, e.g., murine, is well known (see, e.g., Harlow et al., *Antibodies A Laboratory Manual*, Cold Spring Harbor Press, pp. 139-240, 1989, incorporated herein by reference). As it may be difficult to generate human monoclonal antibodies to a human receptor or binding domain polypeptide, it may be desirable to transfer antigen binding regions of non-human monoclonal antibodies, e.g. the $F(ab')_2$ or hypervariable regions or murine monoclonal antibodies, to human constant regions (Fc) or framework regions by recombinant DNA techniques to produce substantially human molecules. Such methods are generally known and are described in, e.g., U.S. Pat. Nos. 4,816,397 and 4,946,778, and EP publications 173,494 and 239,400. Alternatively, one may isolate DNA sequences which code for a human monoclonal antibody or portions thereof that specifically bind to the receptor protein by screening a DNA library from human B cells according to the general protocol outlined in WO 90/14430, and then cloning and amplifying the sequences which encode the antibody (or binding fragment) of the desired specificity.

Usually, polypeptides used for producing antibodies are the full-length receptor or receptor fragments designed from putative extracellular domains identified by a variety of methods known in the art, including computer programs which predict secondary and tertiary structure of a polypeptide based upon its primary amino acid sequence. Another method for designing antigenic peptides utilizes computer programs that predict the high points of hydrophilicity within a particular primary amino acid sequence. For example, using the method of Happ and Woods, *Proc. Natl. Acad. Sci. USA* (1981) 78:3824-3829, via the "Antigen" program in PC/GENE, the inventors identified 3 regions of high hydrophilicity, shown below in Table 7, and used the results to design antigenic peptides to be used in the preparation of antibodies against GBS toxin receptor (see Example 4).

Table 7

High Points of Hydrophilicity in SP55

No.	Ah	Sequence
1	2.05	Glu-Glu-Gly-Ser-Asp-Arg (14-19 of SEQ ID No. 2)
2	1.52	Lys-Asp-Asn-Arg-Thr-Ser (75-80 of SEQ ID No. 2)
3	1.33	Arg-Ala-Pro-Arg-Ala-Glu (25-30 of SEQ ID No. 2)

Ah = Average hydrophilicity.

Antibodies that recognize various portions of the intact GBS toxin receptor can be used to further investigate structure and function of the receptor. The polypeptides of the invention can give rise to antibodies that recognize a variety of forms of GBS toxin receptor, including, but not limited to, intact GBS toxin receptor expressed on a cell surface, denatured GBS toxin receptor or non-denatured GBS toxin receptor, and GBS toxin receptor purified away from cellular components or GBS toxin receptor contained in a cell lysate. GBS toxin receptor antibodies can be used to study species differences as well as GBS toxin receptor expression levels in various cell types.

Antibodies that recognize a portion or all of an extracellular domain are particularly useful as a diagnostic for the monitoring of tumor growth and metastasis, for the detection or identification of a chronic inflammatory condition, such as, for example, rheumatoid arthritis or psoriasis, and for the detection of other medical conditions arising due to hypoxia-driven angiogenesis, such as, for example, restenosis. Typically, such antibodies can be employed in a variety of standard research and diagnostic techniques, including, but not limited to, western blot, immunoprecipitation, ELISA, radioimmunoassay (RIA), BIACOR®, enzyme-linked-immunoassay (EIA), immunofluorescence, fluorescence activated cell sorting (FACS), and *in vivo* diagnostic imaging systems such as magnetic resonance imaging (MRI), nuclear magnetic resonance (NMR), computerized axial tomography (CAT) scan, and position emission tomography (PET), etc.

In addition, antibodies that block the binding of GBS toxin to a GBS toxin receptor can be used for the treatment or prevention of early onset disease in a neonatal human. Such antibodies can directly or indirectly block the GBS toxin binding site on the GBS toxin receptor.

In one embodiment, the GBS toxin receptor protein is naturally occurring and can be isolated from a cell extract by protein purification techniques known in the art, such as, for example, ion exchange column chromatography, high performance liquid chromatography (HPLC), reversed phase HPLC, or affinity chromatography using antibodies that recognize the GBS toxin receptor.

Alternatively, the isolated proteins and polypeptides are expressed using polynucleotides encoding the polypeptide(s) of the invention in operative association with an appropriate control sequence including a promoter in an expression vector suitable for expression, preferably in a mammalian cell, and also in bacterial, insect, or yeast cells.

Usually, the GBS toxin receptor polynucleotide or a fragment thereof can be expressed in a mammalian system. Such expression will usually depend on a mammalian promoter, which is any DNA sequence capable of binding mammalian RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. Usually, a promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence.

This transcription initiation region typically includes an RNA polymerase binding site and a transcription initiation site.

Vectors suitable for replication in mammalian cells are known in the art, and can include viral replicons, or sequences that ensure integration of the sequence encoding PAK65 into the host genome. Suitable vectors can include, for example, those derived from simian virus SV40, retroviruses, bovine papilloma virus, vaccinia virus, and adenovirus.

A suitable vector, for example, is one derived from vaccinia viruses. In this case, the heterologous DNA is inserted into the vaccinia genome. Techniques for the insertion of foreign DNA into the vaccinia virus genome are known in the art, and utilize, for example, homologous recombination. The insertion of the heterologous DNA is generally into a gene which is non-essential in nature, for example, the thymidine kinase gene (tk), which also provides a selectable marker. Plasmid shuttle vectors that greatly facilitate the construction of recombinant viruses have been described (see, for example, Mackett et al. (1984); Chakrabarti et al. (1985); Moss (1987)). Expression of the heterologous polypeptide then occurs in cells or individuals which are immunized with the live recombinant vaccinia virus.

Such suitable mammalian expression vectors usually contain one or more eukaryotic transcription units that are capable of facilitating expression in mammalian cells. The transcription unit is comprised of at least a promoter element to mediate transcription of foreign DNA sequences. Suitable promoters for mammalian cells are known in the art and include viral promoters such as those from simian virus 40 (SV40) (Subramani et al., Mol Cell. Biol. 1:854–864, 1981), cytomegalovirus (CMV) (Boshart et al., Cell 41:521–530, 1985), Rous sarcoma virus (RSV), adenovirus (ADV) (Kaufman and Sharp, Mol. Cell. Biol. 2:1304–1319, 1982), and bovine papilloma virus (BPV), as well as cellular promoters, such as a mouse metallothionein-1 promoter (U.S. Patent No. 4,579,821), a mouse VK promoter (Bergman et al., Proc. Natl. Acad. Sci. USA 81:7041–7045, 1993; Grant et al., Nuc. Acids Res. 15:5496, 1987), and a mouse VH promoter (Loh et al., Cell 33:85–93, 1983).

The optional presence of an enhancer element (enhancer), combined with the promoter elements described herein, will typically increase expression levels. An enhancer is any regulatory DNA sequence that can stimulate transcription up to 1000-fold when linked to endogenous or heterologous promoters, with synthesis beginning at the normal mRNA start site. Enhancers are also active when they are placed upstream or downstream from the transcription initiation site, in either normal or flipped orientation, or at a distance of more than 1000 nucleotides from the promoter (Maniatis et al. (1987) Science 236:1237; Alberts et al. (1989) Molecular Biology of the Cell, 2nd ed.). Enhancer elements derived from viruses can be particularly useful, because they typically have a broader host range. Examples useful in

mammalian cells include the SV40 early gene enhancer (Dijkema et al (1985) EMBO J. 4:761) and the enhancer/promoters derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus (Gorman et al. (1982b) Proc. Natl. Acad. Sci. 79:6777), from human cytomegalovirus (Boshart et al. (1985) Cell 41:521) as well as the mouse μ enhancer (Gillies, Cell 33:717–728, 1983). Additionally, some enhancers are regulatable and become active only in the presence of an inducer, such as a hormone or metal ion (Sassone-Corsi and Borelli (1986) Trends Genet. 2:215; Maniatis et al. (1987) Science 236:1237).

In addition, the transcription unit can also be comprised of a termination sequence and a polyadenylation signal which are operably linked to the GBS toxin receptor coding sequence. Polyadenylation signals include, but are not limited to, the early or late polyadenylation signals from SV40 (Kaufman and Sharp), the polyadenylation signal from the Adenovirus 5 E1B region and the human growth hormone gene terminator (DeNoto et al., Nuc. Acids Res. 9:3719–3730, 1981).

Sequences that cause amplification of the gene may also be desirable, as are sequences which encode selectable markers. Selectable markers for mammalian cells are known in the art, and include, for example, thymidine kinase, dihydrofolate reductase (together with methotrexate as a DHFR amplifier), aminoglycoside phosphotransferase, hygromycin B phosphotransferase, asparagine synthetase, adenosine deaminase, and antibiotic resistant genes such as neomycin.

A GBS toxin receptor, or fragment thereof, can be expressed on the surface of a cell, or can be expressed in soluble or secreted form. Expression on the surface of the cell can be achieved, for example, by including a secretory leader operably linked to a nucleic acid sequence encoding the desired receptor fragment and at least one transmembrane domain. The secretory leader can be that encoded by the GBS toxin receptor gene, or can be a heterologous leader sequence commonly used in the art, such as, for example, the leader sequence of Schizosaccharomyces pombe pho1+ acid phosphatase (Braspenning et al., Biochem Biophys Res. Commun (1998) 245:166-71), the leader sequence of human interleukin-2 (IL-2) gene (Sasada et al., Cell Struct Funct (1988) 13:129-141). Expression in soluble or secreted form can be achieved, for example, by excluding from the gene construct nucleic acid sequences encoding a transmembrane domain. In some instances, solubility and/or secretion are achieved by the use of a fusion partner, such as, for example, chloramphenicol acetyltransferase (CAT), β-galactosidase, and other genes readily expressed in the selected host cell.

The vector that encodes GBS toxin receptor can be used for transformation of a suitable mammalian host cell. Transformation can be by any known method for introducing polynucleotides into a host cell, including, for example packaging the polynucleotide in a virus and transducing a host cell with the virus or by transfection procedures known in the art, as exemplified by U.S. Patent Nos. 4,399,216, 4,912,040, 4,740,461, and 4,959,455 (these patents are incorporated herein by reference).

The transformation procedure used depends upon the host to be transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), N1E-115 (Liles et al., J. Biol. Chem. 261:5307–5313, 1986), PC 12 human hepatocellular carcinoma cells (e.g., Hep G2), and a number of other cell lines, such as insect derived cell lines IF9 and IF21. Cell lines of particular preference are those expressing recombinant GBS toxin receptor constructs constitutively, lines which subsequently develop characteristics of a transformed cell, and lines which more preferably express GBS toxin receptor or fragments on the cell surface. Particularly preferred are ECV cells (a bladder carcinoma cell line originally referred to in the scientific literature as an endothelial cell line), human umbilical vein endothelial cells (HUVEC), bovine, sheep, and human adrenal medulla endothelial cells.

Recombinant GBS toxin receptor or fragments thereof can be produced by culturing host cells expressing the receptor or fragment in a suitable culture medium and under appropriate cell culture conditions. Culture media and conditions are variable depending on the requirements of a particular host cell line and are well known in the art. Typically, cells are cultured at 37°C in a cell culture incubator with a fixed amount of C02, usually in the range of 5-10%.

In another embodiment, the polypeptide fragments can be synthesized chemically by techniques well known in the art, such as solid-phase peptide synthesis (Stewart et al., Solid Phase Peptide Synthesis, W.H. Freeman Co., San Francisco (1963)); Merrifield, J Am Chem Soc 85:2149-2154 (1963)). These and other methods of peptide synthesis are also exemplified by U.S. Patent Nos. 3,862,925, 3,842,067, 3,972,859, and 4,105,602. The synthesis can use manual synthesis techniques or automatically employ, for example, an Applied BioSystems 430A or 431A Peptide Synthesizer (Foster City, California) following the instructions provided in the instruction manual supplied by the manufacturer. It will be readily appreciated by those having ordinary skill in the art of peptide synthesis that the intermediates which are constructed during the course of synthesizing the present analog compounds are themselves novel and useful compounds and are thus within the scope of the invention.

In addition to polypeptides consisting only of naturally-occurring amino acids, peptidomimetics are also provided. Peptide analogs are commonly used in the pharmaceutical industry as non-peptide

drugs with properties analogous to those of the template peptide. These types of non-peptide compounds are termed "peptide mimetics" or "peptidomimetics" (Fauchere, J. (1986) Adv. Drug Res. 15: 29; Veber and Freidinger (1985) TINS p.392; and Evans et al. (1987) J. Med. Chem 30: 1229, which are incorporated herein by reference) and are usually developed with the aid of computerized molecular modeling. Peptide mimetics that are structurally similar to therapeutically useful peptides may be used to produce an equivalent therapeutic or prophylactic effect. Generally, peptidomimetics are structurally similar to a paradigm polypeptide (i.e., a polypeptide that has a biochemical property or pharmacological activity) but have one or more peptide linkages optionally replaced by a linkage selected from the group consisting of: -CH2NH-, -CH2S-, -CH2-CH2-, -CH=CH- (cis and trans), -COCH2-, -CH(OH)CH2-, and -CH2SO-, by methods known in the art and further described in the following references: Spatola, A.F. in "Chemistry and Biochemistry of Amino Acids, Peptides, and Proteins," B. Weinstein, eds., Marcel Dekker, New York, p. 267 (1983); Vol. 1, Issue 3, "Peptide Backbone Modifications" (general review); Morley, J.S., Trends Pharm Sci (1980) pp. 463-468 (general review); Hudson, D. et al., Int J Pept Prot Res (1979) 14:177-185 (-CH2NH-, CH2CH2-); Spatola, A.F. et al., Life Sci (1986) 38:1243-1249 (-CH2-S); Hann, M.M., J Chem Soc Perkin Trans I (1982) 307-314 (-CH-CH-, cis and trans); Almquist, R.G. et al., J. Med Chem (1980) 23:1392-1398 (-COCH2-); Jennings-White, C. et al., Tetrahedron Lett (1982) 23:2533 (-COCH2-); Szelke, M. et al., European Appln. EP 45665 (1982) CA: 97:39405 (1982) (-CH(OH)CH2-); Holladay, M.W. et al., Tetrahedron Lett (1983) 24:4401-4404 (-C(OH)CH2-); and Hruby, V.J., Life Sci (1982) 31:189-199 (-CH2-S-); each of which is incorporated herein by reference. A particularly preferred non-peptide linkage is -CH2NH-. Such peptide mimetics may have significant advantages over polypeptide embodiments, including, for example: more economical production, greater chemical stability, enhanced pharmacological properties (half-life, absorption, potency, efficacy, etc.), altered specificity (e.g., a broad-spectrum of biological activities), reduced antigenicity, and others. Labeling of peptidomimetics usually involves covalent attachment of one or more labels, directly or through a spacer (e.g., an amide group), to non-interfering position(s) on the peptidomimetic that are predicted by quantitative structure-activity data and/or molecular modeling. Such non-interfering positions generally are positions that do not form direct contacts with GBS toxin (e.g., are not contact points in the GBS toxin binding domain of the GBS toxin receptor). Derivitization (e.g., labelling) of peptidomimetics should not substantially interfere with the desired biological or pharmacological activity of the peptidomimetic.

Systematic substitution of one or more amino acids of a consensus sequence with a D-amino acid of the same type (e.g., D-lysine in place of L-lysine) may be used to generate more stable peptides. In addition, constrained peptides comprising a consensus sequence or a substantially identical consensus

sequence variation may be generated by methods known in the art (Rizo and Gierasch (1992) Ann. Rev. Biochem. 61: 387, incorporated herein by reference); for example, by adding internal cysteine residues capable of forming intramolecular disulfide bridges which cyclize the peptide.

The invention also provides a complex comprising a GBS toxin bound to a mammalian GBS toxin receptor or a fragment of a mammalian GBS toxin receptor. Preferably, the complex comprises a GBS toxin bound to a GBS toxin receptor polypeptide described above that can bind GBS toxin. Typically, a complex is formed by contacting a GBS toxin with such a polypeptide under conditions that permit specific binding of the GBS toxin to the polypeptide. The GBS toxin can be labeled or unlabeled. The polypeptide can be present on the surface of a cell, or immobilized in a well or on a bead, or the polypeptide can be present in solution.

DETECTION METHODS

Yet another aspect of the invention provides methods for detecting or monitoring a variety of medical conditions characterized by pathologic and/or hypoxia-driven angiogenesis or neovascularization. Examples include, but are not limited to, early onset disease in the neonate, and the progression of cancers involving tumors.

Early onset disease can be diagnosed by detecting the presence or absence of GBS toxin in a patient. One method of detection is a competition assay that determines the effect of a suspected sample on the formation of a complex between GBS toxin and a GBS toxin receptor or fragment thereof. For example, the method comprises contacting a control GBS toxin with a GBS toxin receptor polypeptide, in the presence and absence of a sample suspected of containing GBS toxin and under conditions that permit specific binding of the GBS toxin to the polypeptide, and comparing the amount of complex formation achieved in the presence of the suspected sample to the amount of complex formation achieved in the absence of the suspected sample. Preferably, the control GBS toxin is substantially purified and of a known concentration. Preferably, the control GBS toxin further comprises a label. Suitable labels include, but are not limited to, radioisotopes, chromophores, fluorophores, biotin, avidin, and other labels used by one skilled in the art. Another method directly measures, rather than by competition with a control GBS toxin, complex formation between GBS toxin present in a suspected sample and a GBS toxin receptor polypeptide.

Pathologic vasculature can be detected in a mammalian tissue by detecting the presence or absence of GBS toxin receptor in the region of a tumor, with the presence of GBS toxin receptor being indicative of the presence of pathologic vasculature. The method can be used to monitor tumor growth or metastasis. One method of detection involves the use of molecules, e.g. antibodies, that specifically

bind to a GBS toxin receptor, preferably an extracellular domain of GBS toxin receptor. Typically, the method comprises administering, to a mammalian tissue, e.g. in a mammal having a cancerous tumor, e.g., an antibody that recognizes a GBS toxin receptor, and detecting specific binding of the antibody. Typically, the antibody is a labeled antibody. Preferably, the observations are quantitative and can be visual.

During surgery, the margin of a tumor can be visualized by any of a number of imaging techniques known in the art and described above. The imaging of the tumor is effected by detecting the binding of a labeled antibody or other molecules to the GBS toxin receptor on the pathologic vasculature of a tumor. This type of surgery is also known as virtual surgery because while performing the surgery, the surgeon views the tumor indirectly on an imaging screen.

DRUG DISCOVERY

A fourth aspect of the invention provides methods, using the polypeptides of the invention, of identifying drug candidates for the treatment of medical conditions characterized by hypoxia-driven angiogenesis or neovascularization. Preferred compounds are competitive inhibitors of GBS toxin binding to a GBS toxin receptor or inhibit GBS toxin receptor activity. Particularly preferred are compounds that inhibit the first phosphorylation step in the signal transduction pathway. Compounds can be produced by a variety of random drug design methods commonly known in the art, such as, for example, combinatorial chemistry (U.S. Patent No. 5,646,285; U.S. Patent No. 5,639,603), peptide libraries (U.S. Patent No. 5,591,646; U.S. Patent No. 5,367,053; U.S. Patent No. 5,747,334), phage display (U.S. Patent No. 5,403,484; U.S. Patent No. 5,223,409), SELEX® (U.S. Patent No. 5,773,598; U.S. Patent No. 5,763,595; U.S. Patent No. 5,763,566), and combinatorial carbohydrate chemistry (Hirschmann et al., J Med Chem (1996) 39:2441-2448; Hirschmann et al., J Med Chem (1998) 41:1382-1391; Sofia MJ, Mol Divers (1998) 3:75-94; U.S. Patent No. 5,780,603; U.S. Patent No. 5,756,712)

An alternative approach is rational drug design with the intent of producing a GBS toxin mimetic or a GBS toxin receptor mimetic with improved therapeutic properties using techniques such as x-ray crystallography, nuclear magnetic resonance (NMR) correlation spectra (U.S. Patent No. 5,698,401), computer assisted molecular modeling (U.S. Patent No. 5,579, 250; U.S. Patent No. 5,612,895; U.S. Patent No. 5,680,331, Cooper et al., J. Comput.-Aided Mol. Design, 3:253-259 (1989); Brent et al., J. Comput.-Aided Mol. Design 2:311-310 (1988)) and other methods of rational drug design known in the art. **FIG. 1** provides a broad overview of some of the main steps in some of the rational drug design methods of the present invention. For example, one approach to rational drug design involves a computer program, such as INSIGHTII (available from Bisoym Technologies, 10065 Barnes Canyon

Road, San Diego, California) to identify active sites in proteins by homology-based modeling. This method facilitates the modeling of a protein by using a similar protein whose structure is well known. Commercial software containing search algorithms for three dimensional database comparisons are available from vendors such as Day Light Information Systems, Inc., Irvine, California 92714, and Molecular Design Limited, 2132 Faralton Drive, San Leandro, California 94577.

In one embodiment, the compound can bind the GBS toxin receptor and induce an inflammatory response in a manner similar to the binding of GBS toxin to the GBS toxin receptor. Such compounds can be used, for example, as a drug to target an inflammatory response to the developing vasculature of a tumor.

In another embodiment, the compound can bind the GBS toxin receptor with or without inducing an inflammatory response, preferably without inducing an inflammatory response. In one instance, the compound can be used as a vehicle to target pathological neovasculature for treatment with a cytotoxic agent. For example, the cytotoxic agent can be chemically coupled to the compound to form a chimeric drug. Such chimeric drugs can be used in the treatment of tumors, rheumatoid arthritis, wound healing, spinal cord injury, and other conditions characterized by hypoxia-driven angiogenesis or neovascularization. In another instance, the compound can be used directly to competitively inhibit binding of GBS toxin to a GBS toxin receptor. Such compounds can be used in the treatment of early-onset disease in the neonate.

In a third embodiment, the compound can bind GBS toxin and can be used in the treatment of early-onset disease in the neonate.

The polynucleotides of the invention can be expressed in random mutagenesis systems such as phage display or the yeast two-hybrid system for the synthesis and identification of mutant peptide GBS toxin receptor polypeptides that bind GBS toxin. Alternatively, immobilized or soluble GBS toxin receptor fragments of the invention can be used to screen combinatorial peptide and combinatorial chemical libraries and non-random recombinant and synthetic peptides and other compounds (such as non-peptide molecules) for GBS toxin receptor binding. Compounds that bind GBS toxin or GBS toxin receptor can then be further characterized in a functional assay for any of the activities described above in order to identify a drug candidate for the treatment of medical conditions involving angiogenesis or neovascularization.

A compound which inhibits binding of GBS toxin to a GBS toxin receptor can be identified by combining a test compound with a mammalian GBS toxin receptor or fragment thereof capable of binding GBS toxin, under conditions that permit specific binding of GBS toxin to the GBS toxin receptor or fragment, and determining the amount of inhibition by the compound of the binding of GBS toxin to

the GBS toxin receptor or fragment.

In a preferred embodiment, the GBS toxin receptor or fragment is expressed by a cell, preferably on the cell surface. The cells are contacted with labeled GBS toxin in the presence or absence of the test compound. A change in the binding of GBS toxin to the GBS toxin receptor is then determined. Alternatively, the GBS toxin is unlabeled and an antibody that recognizes GBS toxin is labeled instead. The labeled antibody is used to measure inhibition by a compound of GBS toxin binding to the GBS toxin receptor or fragment. In another embodiment, the GBS toxin receptor or fragment is not associated with a cell, but is instead coupled to a matrix, such as, for example, a well in a microtiter plate or a bead. Additional suitable solid supports include latex, polystyrene beads (Interfacial Dynamics Corp. Portland, Oreg.), magnetic particles (Advanced Magnetics, Cambridge, Mass.) and nylon balls (Hendry et al., *J. Immunological Meth.,* 35:285–296, 1980). The receptor or fragment can be coupled to the matrix directly or indirectly through an antibody, coupled to the matrix, that binds the receptor fragment. In a third embodiment, the GBS toxin receptor or fragment is soluble and can be immunoprecipitated with an antibody that recognizes the receptor or fragment.

A preferred method for identifying a compound which binds a mammalian GBS toxin receptor comprises the steps of (1) combining a test compound with a GBS toxin receptor or fragment thereof under conditions that allow specific binding to occur, and (2) detecting a complex formed between the test compound and the GBS toxin receptor or fragment. A preferred method is a competition assay which determines the ability of the test compound to compete for binding to the GBS toxin receptor or fragment. In such an assay, GBS toxin is combined with the GBS toxin receptor or fragment in the presence or absence of the test compound. Decreased specific binding of GBS toxin in the presence versus the absence of the test compound is indicative of the ability of the test compound to bind a mammalian GBS toxin receptor. Another method comprises combining a control compound with the GBS toxin receptor or fragment under the same conditions as the test compound and comparing the amount of complex formation between the test compound or the control compound and the GBS toxin receptor or fragment thereof. Preferably, the test compound and/or the control compound are labeled. The test compound can be any of a number of classes of compounds, such as for example, small organic molecules (such as those used for and obtained by combinatorial chemistry), polysaccharides, polypeptides, RNA, antibodies, and single chain antibodies. In a preferred embodiment, the polypeptide is expressed by a cell, preferably on the surface of the cell, and preferably by a stable transfected cell. Such a system is particularly useful for testing the effectiveness of a chimeric compound comprising a cytotoxic agent. The cytotoxic activity of the compound can be determined by exposing a cell expressing the GBS toxin receptor on the cell surface to the test chimeric compound and detecting signs

of cytotoxicity. One could detect such signs by a viability stain of the cell, by detecting apoptosis (for example, by a DNA ladder assay or a TUNEL™ stain, which binds to broken DNA), by measuring tritiated thymidine incorporation into the cell, and by quantitating kinase-dependent phosphorylation (e.g., using phosphoantibodies or various phosphoimaging techniques).

In another embodiment, the invention provides a method for identifying an inhibitor of GBS toxin receptor. The method comprises incubating test cells in the presence and absence of a test compound. The test cells express GBS toxin receptor or a fragment thereof having GBS toxin receptor activity (e.g., a fragment that increases the proliferation or migration of the expressing cells relative to control cells of the same cell type that do not express the fragment). The test cells are incubated under conditions in which the cells incubated in the absence of the test compound can proliferate or migrate. Control cells that do not express the GBS toxin receptor or fragment proliferate or migrate less than cells that express the GBS toxin receptor or fragment. The proliferation or migration (also referred to herein as motility) of the test cells incubated in the presence or absence of the test compound is compared. Less proliferation or migration in the presence of the test compound than in the absence of the test compound is indicative of the test compound being an inhibitor of the GBS toxin receptor. Preferably, as a control to determine whether the test compound specifically inhibits the GBS toxin receptor, the proliferation or migration of control cells in the presence and absence of the test compound is also compared. In the absence of a difference in the proliferation or migration of control cells incubated in the presence or absence of the test compound, decreased proliferation or migration in test cells exposed to the test compound relative to test cells not exposed to the test compound is indicative of specific inhibition of the GBS toxin receptor. It will be readily apparent that the control portions of the method need not be performed contemporaneously with the test portions of the method. For example, control cells can be incubated with a battery of test compounds to determine cellular effects of the test compounds prior to incubating the test cells with the test compounds. Motility or migration can be determined by detecting movement of cells on a culture dish. Proliferation can be detected in a number of ways, including, but not limited to, measuring tritiated thymidine incorporation, cell counts, apoptosis assays, and viability assays. Preferred cells include cells transfected with GBS toxin receptor, preferably endothelial cells transfected with GBS toxin receptor, even more preferably vascular endothelial cells or microvascular endothelial cells. Primary cells that express GBS toxin receptor are also preferred, for example, endothelial cells that have been passaged in cell culture, at confluence, no more than 8 or 9 times. A preferred class of test compounds includes kinase inhibitors, preferably cAMP-dependent kinase inhibitors, PKC inhibitors, and CK2 inhibitors, which can be used as a starting point for developing more specific GBS toxin receptor inhibitors. Another class of compounds includes antibodies specific for

GBS toxin receptor. Particularly preferred are single chain antibodies, preferably a collection of single chain antibodies that recognize various epitopes on the GBS toxin receptor. Less preferred are divalent antibodies specific for the binding site of the GBS toxin receptor ligand because they may trigger the signal transduction cascade upon dimerization.

Another embodiment of the invention is a method of identifying an inhibitor of endothelial cell proliferation or migration, which are essential components of angiogenesis. The method basically comprises the steps described in the preceding paragraph and uses endothelial cells.

Yet another embodiment of the invention is a method of identifying a therapeutic compound for the treatment or prevention of a medical condition characterized by pathologic or hypoxia-driven angiogenesis or neovascularization. The method basically comprises the steps described above and uses cells from tissues derived from mammals afflicted with the medical condition or cells that serve as a model for afflicted tissue.

A preferred method for designing a compound which inhibits binding of a GBS toxin to a mammalian GBS toxin receptor comprises (1) simulating and selecting the most probable conformations of a GBS toxin receptor or fragment thereof, (2) designing a chemically modified analog that substantially mimics the energetically most probable three-dimensional structure of the GBS toxin receptor or fragment, (3) chemically synthesizing the analog, and (4) evaluating the bioactivity of the analog. Preferably, steps (a) and (b) are performed with the aid of a computer program.

A preferred method for designing a compound which binds to a mammalian GBS toxin receptor comprises (1) simulating and selecting the most probable conformations of a GBS toxin receptor or fragment thereof, (2) deducing most probable binding domains of the receptor or fragment, (3) designing a compound that would form the energetically most probable complexes with the receptor or fragment, (4) chemically synthesizing the compound, and (5) evaluating the bioactivity of the compound. Preferably, steps (a)-(c) are performed with the aid of a computer program.

Preferred polypeptides for use in the screening assays described above are polypeptides sharing at least about 85% identity, preferably at least about 95% identity, and most preferably greater than about 99% identity with the amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 4, or a fragment thereof having GBS toxin receptor activity. Most preferred are polypeptides having an amino acid sequence of SED ID NO: 2, 4 OR 8 or a fragment thereof having GBS toxin receptor activity.

METHODS OF PURIFICATION

Another aspect of the invention is a method for purifying a compound that binds a GBS toxin receptor, for example, natural ligand, other polysaccharides, or an antibody specific for the GBS toxin

receptor. The method comprises providing a polypeptide comprising a mammalian GBS toxin receptor or fragment thereof that binds GBS toxin, contacting the polypeptide with a sample comprising the compound under conditions that allow specific binding of the compound to the polypeptide, and separating the bound compound from the remainder of the sample. The polypeptide can be soluble but preferably is immobilized on a substrate e.g., on a bead, membrane or on the surface of a cell, preferably a stable transfected cell.

METHODS OF TREATMENT

GBS toxin receptor polypeptides and antibodies that interfere with GBS toxin binding can be used in a method of treatment of the human or animal body. For example, such inhibitors of GBS toxin binding can be administered to a patient to treat or prevent medical conditions involving GBS toxin binding to a GBS toxin receptor, such as, for example, early onset disease in the neonate.

GBS toxin mimetics or other compounds that bind and/or inhibit GBS toxin receptor, some of which can be identified by the drug discovery assays of the invention, can be used in a method of treatment of the human or animal body or can be used for the manufacture of a medicament for the treatment or prevention of any of a number of medical conditions involving pathologic and/or hypoxia-driven angiogenesis, such as, for example, cancerous tumors, chronic inflammatory diseases, scarring during wound healing or repair of neural injury.

In a preferred embodiment, such a compound exerts its therapeutic effect by binding GBS toxin receptor and evoking an inflammatory response, as does GBS toxin. Preferably, such compounds comprise a sulfhydryl, hydroxyl, or amino group displayed so as to be available for binding complement C3.

In another preferred embodiment, the compound is an inhibitor of GBS toxin activity. Preferred inhibitors include, but are not limited to, kinase inhibitors, single chain antibodies specific for the GBS toxin receptor, and antisense polynucleotides that specifically hybridize under high stringency conditions to a GBS toxin receptor nucleic acid sequence, such as that of SEQ ID NO:1, SEQ ID NO:3 or SEQ ID NO:7.

In another preferred embodiment, the compound exerts its therapeutic effect without evoking an inflammatory response. The compound can be used to deliver a cytotoxic agent to tissue in close proximity to a cell expressing a GBS toxin receptor, such as, for example, a tumor undergoing angiogenesis. Preferably, the compound is covalently attached to a cytotoxic agent and can be associated non-covalently with a cytotoxic agent, such as, for example, on the external surface of a liposome, micelle, or other lipophilic drug encapsulating structure. Preferred cytotoxic agents include antineoplastic agents commonly known in the art, such as, for example, mechlorethamine, chlorambucil,

cyclophosphamide, melphalan, ifosfamide, and other alkylating agents, methotrexate and other folate antagonists, 6-mercaptopurine and other purine antagonists, 5-fluorouracil and other pyrimidine antagonists, cytarabine, ovinblastine, vincustine, and other vincas, etoposide and other podophyllotoxins, doxorubicin, bleomycin, mitomycin, and other antibiotics, carmustine, lomustine and other nitrosureas, cisplatin, interferon, asparaginase, tamoxifen, flutamide, and taxol. Other preferred biologic agents include sense and/or antisense RNA or DNA sequences derived from specific tumor promoter or suppressor genes, such as, for example, the p53 and TGF gene families, signal transduction protein family members such as, for example, ras and myc, and growth factor receptor kinases such as, for example flt2 and flk1, Tai1, Tai2, and neuropholin, and other genes implicated in neoplastic disease and other diseases driven by pathologic angiogenesis.

In another embodiment, GBS toxin receptor polypeptide or fragment thereof can be administered to a subject as a decoy to reduce the amount of stimulation of the GBS toxin receptor present in afflicted tissues (e.g., tumor tissues), thereby reducing cellular responses leading to proliferation and migration of cells of the afflicted tissues. Preferably, the GBS toxin receptor polypeptide or fragment is administered in soluble form, even more preferably sans transmembrane domains.

Pharmaceutical Compositions

Polypeptides of the invention that comprise a domain essential for GBS toxin binding that have the desired characteristics for bioavailability, stability and other important parameters of pharmacokinetics *in vivo* can be used as a competitive inhibitor of GBS toxin binding for medical conditions, such as, for example, early onset disease in the neonate, in which GBS toxin binding is undesirable. Appropriate polypeptides can include fragments having an amino acid sequence corresponding to a partial or full sequence of SEQ ID NO: 2 or SEQ ID NO: 4 or analogs thereof.

Compounds determined by assays using the polypeptides of the invention to bind and/or GBS toxin receptor and/or induce an inflammatory response, and that have the desired pharmacokinetic characteristics, can be used as treatments for medical conditions in which GBS toxin binding can be therapeutic, such as, for example, medical conditions involving pathologic or hypoxia-driven angiogenesis or neovascularization.

Pharmaceutical compositions of the invention include a pharmaceutically acceptable carrier that may contain a variety of components that provide a variety of functions, including regulation of drug concentration, regulation of solubility, chemical stabilization, regulation of viscosity, absorption enhancement, regulation of pH, and the like. For example, in water soluble formulations the pharmaceutical composition preferably includes a buffer such as a phosphate buffer, or other organic

acid salt, preferably at a pH of between about 7 and 8. Other components may include antioxidants, such as ascorbic acid, hydrophilic polymers, such as, monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, dextrins, chelating agents, such as EDTA, and like components well known to those in the pharmaceutical sciences, e.g. Remington's Pharmaceutical Science, latest edition (Mack Publishing Company, Easton, PA).

An effective amount of an active compound such as a GBS toxin receptor polypeptide, mimetic or analog, or GBS toxin mimetic or analog for particular applications depends on several factors, including the chemical nature of the polypeptide, mimetic or analog, the disorder being treated, the method of administration, and the like. Preferably, an effective amount will provide a concentration of polypeptide or mimetic of between about 0.0001 to 100 μM at the target GBS toxin receptor on a cell surface, more preferably less than 10 μM, with less than 1 μM being most preferred.

The active compound can be administered to a mammalian host in a variety of forms, i.e., they may be combined with various pharmaceutically acceptable inert carriers in the form of tablets, capsules, lozenges, troches, hard candies, powders, sprays, elixirs, syrups, injectable or eye drop solutions, and the like depending on the chosen route of administration, e.g., orally or parenterally. Parenteral administration in this respect includes administration by the following routes: intravenous, intramuscular, subcutaneous, intraocular, intrasynovial, transepithelial (including transdermal, ophthalmic, sublingual and buccal), topical (including ophthalmic, dermal, ocular, rectal, nasal inhalation via insufflation and aerosol), and rectal systemic.

The active compound may be orally administered, for example, with an inert diluent or with an assimilable edible carrier, it may be enclosed in hard or soft shell gelatin capsules, compressed into tablets, or incorporated directly with the food of the diet. For oral therapeutic administration, the active compound may be incorporated with excipient and used in the form of ingestible tablets, buccal tablets, troches, capsules, elixirs, suspensions, syrups, wafers, and the like. Such compositions and preparations should contain at lease 0.1% of active compound. The percentage of the compositions and preparations may, of course, be varied and may conveniently be between about 2% to about 6% of the weight of the unit. The amount of active compound in such therapeutically useful compositions is such that a suitable dosage will be obtained. Preferred compositions or preparations according to the present invention are prepared so that an oral dosage unit form contains between about 1 and 1000 mg of active compound.

Tablets, troches, pills, capsules and the like may also contain the following: a binder such as polyvinylpyrrolidone, gum tragacanth, acacia, sucrose, corn starch or gelatin; an excipient such as calcium phosphate, sodium citrate and calcium carbonate; a disintegrating agent such as corn starch, potato starch, tapioca starch, certain complex silicates, alginic acid and the like; a lubricant such as

sodium lauryl sulfate, talc and magnesium stearate; a sweetening agent such as sucrose, lactose or saccharin; or a flavoring agent such as peppermint, oil of wintergreen or cherry flavoring. Solid compositions of a similar type are also employed as fillers in soft and hard-filled gelatin capsules; preferred materials in this connection also include lactose or milk sugar as well as high molecular weight polyethylene glycols. When the dosage unit form is a capsule, it may contain, in addition to materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar or both. A syrup or elixir may contain the active compound, sucrose as a sweetening agent, methyl and propylparabens as preservatives, a dye, flavoring such as cherry or orange flavor, emulsifying agents and/or suspending agents, as well as such diluents as water, ethanol, propylene glycol, glycerin and various combinations thereof. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compound may be incorporated into sustained-release preparations and formulations.

The active compound may also be administered parenterally or intraperitoneally. For purposes of parenteral administration, solutions in sesame or peanut oil or in aqueous propylene glycol can be employed, as well as sterile aqueous solutions of the corresponding water-soluble, alkali metal or alkaline-earth metal salts previously enumerated. Such aqueous solutions should be suitably buffered, if necessary, and the liquid diluent first rendered isotonic with sufficient saline or glucose. Solutions of the active compound as a free base or a pharmacologically acceptable salt can be prepared in water suitably mixed with a surfactant such as hydroxypropylcellulose. A dispersion can also be prepared in glycerol, liquid polyethylene glycols and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal injection purposes. In this connection, the sterile aqueous media employed are all readily obtainable by standard techniques well-known to those skilled in the art.

The pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, liquid polyethylene glycol and the like), suitable mixtures thereof, and vegetable oils. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of

the required particle size in the case of a dispersion and by the use of surfactants. The prevention of the action of microorganisms can be brought about by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal and the like. In many cases it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by use of agents delaying absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions are prepared by incorporating the active compound in the required amount in the appropriate solvent with various of the other ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the sterilized active ingredient into a sterile vehicle which contains the basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and the freeze drying technique which yield a powder of the active ingredient plus any additional desired ingredient from the previously sterile-filtered solution thereof.

For purposes of topical administration, dilute sterile, aqueous solutions (usually in about 0.1% to 5% concentration), otherwise similar to the above parenteral solutions, are prepared in containers suitable for drop-wise administration to the eye. The compounds of this invention may be administered to a mammal alone or in combination with pharmaceutically acceptable carriers. As noted above, the relative proportions of active ingredient and carrier are determined by the solubility and chemical nature of the compound, chosen route of administration, the particular compound chosen and the physiological characteristics of the particular patient under treatment.

KITS

Yet another aspect of the invention is a kit for use in carrying out any of the above methods. A preferred embodiment is a kit comprising a GBS toxin receptor or fragment thereof. Preferably, the receptor or fragment is immobilized. A preferred kit can be used for identifying a compound that binds to GBS toxin receptor, and comprises at least one cell that expresses GBS toxin receptor.

Another embodiment is a kit for monitoring tumor growth or metastasis, comprising a reagent for detecting expression of a GBS toxin receptor. Examples of such reagents include, but are not limited to, polynucleotide probes that hybridize to a GBS toxin receptor nucleic acid sequence and compounds that bind to a GBS toxin receptor, such as, for example, an antibody that specifically recognizes GBS toxin receptor, a GBS toxin, a GBS toxin mimetic, or other compounds identified by the screening methods described above.

A third embodiment is a kit for purifying a compound that binds a GBS toxin receptor, comprising a GBS toxin receptor or fragment thereof that binds the compound. Preferred compounds include GBS toxin, GBS toxin mimetics, antibodies that specifically bind GBS toxin receptor, and other compounds identified by the screening methods described above.

Additional kit components can include, but are not limited to, additional reagents required for detection, a reference standard(s), instructions for use, and the like. Suitable reference standards include positive controls, negative controls, photographs of such controls, tabulated or graphed data of such controls, and the like. The kits may further comprise instructions for carrying out the methods described above, preferably printed instructions.

EXAMPLES

EXAMPLE 1 - CLONING SHEEP GBS TOXIN RECEPTOR

Primary culture of sheep lung endothelial cells

Small pieces of primary lung tissues from a 7-week old sheep are cut into small pieces in Hank's balanced salt solution (HBSS) containing 10 mM HEPES buffer (Life Technology), 1% penicillin/streptomycin and 0.1% gentamycin, and are cultured in sheep lung complete medium (Life Technology) at 37°C. After one week of the culture, clones of sheep lung endothelial cells are identified by Cobblestone morphology and harvested into 24-well tissue culture plates (Falcon) using cloning rings. When the cells are confluent, they are detached by pancreatin and transferred to a 60-mm tissue culture Petri dish or a T-25 tissue culture flask (Falcon). When they are confluent again, they are split and cultured into a few 100-mm tissue culture plates (Falcon). Each split is considered to be one passage. The same procedure is repeated until enough cells ($\sim 10^8$) are obtained for isolation of mRNA.

Isolation of mRNA and construction of cDNA library

Poly(A)+ RNA is isolated from 9.2×10^7 sheep lung endothelial cells (passage 8 and 9) by a standard method (Pharmacia). A total of 16 μg poly(A)$^+$ RNA is acceptable amount obtained. 2.5 μg mRNA can be used to construct a cDNA library. Poly(A)$^+$ RNA is oligo(dT)-primed (with *Not* I restriction site) and converted into double-stranded cDNA. After adding a *BstX* I/*EcoR* I adaptor, the cDNA is unidirectionally cloned into the *BstX* I and *Not* I sites of pCDNA3.1(+) (Invitrogen). *E. coli* Top10F' (Invitrogen) is used as a host strain for amplification. 5.38×10^6 primary clones are an acceptable number generated. The library is amplified by plating cells onto fifty large LB agar plates containing ampicillin (100 μg/ml). The plates are scraped and aliquoted so that each aliquot represents 10 plates. DNA is purified by Qiagen Max columns (Qiagen).

Screening of cDNA library for a gene encoding GBS toxin receptor

To screen a cDNA library for a gene encoding GBS toxin receptor gene, a unique colorimetric method is used. Five μg plasmid DNA from each pool of cDNA library is used to transfect COS7 cells. The transfected cells are cultured in four to eight 96-well tissue culture plates (Falcon) for transient expression. Each well contains about 20,000 transfected cells in DMEM medium (Life Technology). COS7 cells transfected with pCDNA3.1(+) are used as a control. After 3 days expression, the medium is carefully removed. Each well is rinsed 3 times with HPSS buffer containing Mg^{2+} and Ca^{2+} (wash buffer) (Life Technology).

The cells are then incubated with biotinylated toxin (50μ*l* per well; 1 to 1.5 μg/ml) at room temperature for 1 h. After the hour incubation, the biotinylated toxin is discarded and the wells are rinsed 3 times with the wash buffer. The cells are incubated with streptavidin-ß-gal solution and each well is rinsed 3 times with the wash buffer. The cells are then incubated with PNPG (50 μl per well; 1 mg/ml in substrate buffer) at 37°C. Absorbance at 405 nm is measured by an ELISA reader at 1 and 20 h, respectively. The cells which give the highest OD are harvested. Plasmid DNA is isolated by Hirt extraction. Plasmid DNA is amplified in *E. coli* to have enough DNA for the next transfection (enrichment).

Enrichment is done 8 times by this colorimetric method. The number of the transfected cells loaded into each well is gradually decreased in the last few enrichments and untransfected cells are added to each well to give a total number of 20,000 cells per well for the cells to be confluent and to reduce background after 3 days' expression. At the last enrichment, each well has only 1 to 10 transfected cells. Cells giving the highest OD are harvested. DNA is isolated and amplified in *E. coli*.

A number of isolated clones are individually assayed by this colorimetric method. The clones which showed higher binding to CM101 are sequenced.

Sequence analysis

DNA sequence analysis of clone pFU102, which has a 2.1kb insert, revealed a sequence encoding a partial integral glycoprotein. N-terminal sequence was obtained by 5'RACE method (Life Technology) and a full-length gene is designated as SP55. Triple ligation yielded pCD55, which contains an entire coding region of SP55.

mRNA for the SP55 has 2844 nucleotides, encoding a protein of 495 amino acids with a predicated mass of 55 KDa, SP55. Analysis by the method of Klein et al. (Klein et al., *Biochim Biophys Acta*, 815:468-476 (1985)) classifies SP55 as an integral protein with seven transmembrane segments. SP55 has both N-glycosylation and kinase phosphorylation sites. A Swiss-Prot. search of SP55 did not reveal any high homology to known human proteins. However, SP55 has some identity (~ 30%) to renal

sodium-dependent phosphate transporters from human, rabbit, mouse and rat. In addition, SP55 has some identity (~ 30 to 39%) to hypothetical proteins (HYP50 and HYP63) from *C. elegans*.

EXAMPLE 2 - CLONING HUMAN GBS TOXIN RECEPTOR

The sheep GBS toxin receptor sequence shares about 37% identity with HYP50 and about 33% identity to HYP63, two hypothetical proteins from *C. elegans*. In the regions corresponding to amino acid residues 180-186 and 443-449 of SEQ ID No. 2, five amino acids within a seven amino acid stretch are absolutely conserved among the three proteins.

A first degenerate oligonucleotide, CMR3-S: 5'-CGGGATCCCGCCNGCNATGCAYRSHRTSTGG-3'(SEQ ID No. 5), was designed to include all possible codons encoding the amino acid sequences of SP55, HYP50, and HYP63 in the 180-186 region. A second degenerate oligonucleotide, CMR4-AS2: 5'-GGAATTCCDGGDGCRATKTCNARRTRRTT-3' (SEQ ID No. 6), was designed to include the complementary sequences of all possible codons encoding the amino acid sequences of SP55, HYP50, and HYP63 in the 443-449 region.

Polymerase chain reaction (PCR) was conducted using these oligonucleotides and a human embryo lung cDNA library as a template. The reaction yielded three overlapping sequences approximately 400 bp in size, which encompass part of the nucleic acid sequence of SEQ ID No. 3. These sequences were then used as probes to clone the remainder of the gene, referred to herein and HP59 (SEQ ID NO: 7).

EXAMPLE 3 - PREPARATION OF ANTIBODIES AGAINST GBS TOXIN RECEPTOR

Rabbits are immunized with the synthetic peptides shown in Table 8. A 1 mg/ml solution of peptide plus KLH in 0.01M phosphate buffer is prepared. For the first immunization, 200 μg of peptide plus KLH (200 μl) and an equal volume of Freunds complete adjuvant, emulsified well before injection, is injected into 3-4 spots on the dorsal surface about the neck and shoulders of a rabbit. After two weeks, the second immunization (boost) is given at the same concentration of immunogen, but emulsified in Freunds incomplete adjuvant. The boost is delivered in the same region of the body. After another two weeks, blood is collected and assayed by ELISA for response against the peptide without KLH. Further boosts are given to improve antibody titer, if necessary.

Table 8

Immunogenic Peptides

Peptide	Amino Acid Sequence	Size	SEQ ID Ref.
p56a	APSDGEEGSDRTPLLQRAPRAEPAPVC	27 aa	residues 8-35 of SEQ ID NO:4
p55a	LAPSDGEEGSDRTPL	15 aa	residues 7-22 of SEQ ID NO: 4
p57a	NTTAKDNRTSYECA	14 aa	residues 71-84 of SEQ ID NO: 4

Peptide p55 is a fragment of an extracellular domain of GBS toxin receptor. Peptide p57a is a fragment of an intracellular domain of GBS toxin receptor. Animals immunized with these peptides produce polyclonal antibodies Pab55 and Pab57, respectively.

EXAMPLE 4 – DETECTION OF GBS TOXIN RECEPTOR EXPRESSION IN TUMOR CELLS

This example shows that GBS toxin receptor can be detected in tumor cells. Immunohistochemistry is performed on paired human and mouse tissues of normal or tumor origin, using rabbit polyclonal antibodies Pab 55 and Pab 57.

Mouse and human tumor tissues are fixed in 10% neutral formalin. The tissues are then dehydrated, paraffin embedded and 10-20 x 8-micron sections are cut for immunohistochemical staining.

Immunohistochemical analysis is performed with the automated Ventana Immunohistochemical Stainer according to the manufacturer's suggested protocol (Ventana, Tucson, Arizona). Sections are deparaffinated with xylene. The prepared sections are then treated with 1% hydrogen peroxide prepared in 30% aqueous methanol for 20 minutes at room temperature to quench endogenous peroxidase activity. The slides are then washed with PBS, blocked with 5% BSA and 5% goat serum in PBS, washed again and then incubated for 30 minutes at 37°C with the appropriate diluted (1:100) antibody. Horseradish peroxidase-labeled goat anti-rabbit IgG is used as a secondary antibody. For visualization, the sections are incubated with DAB/H_2O_2. The sections are finally incubated with a copper enhancer (Ventana) for 4 minutes, washed, counterstained with hematoxylin, and mounted in toluene-minus mounting medium. Photographic documentation is performed and images are stored for later review and analysis. The results are summarized in Table 9. The numbers refer to glass slides.

TABLE 9

Immunohistochemistry of tumor and normal tissues

(diff. = differentiated)

Human tissues:

	Antibody	Magnification	Signal
1. Ovary tumor (95-02VO16) high grade papillary carcinoma	Pab 55	400x	+
2. Ovary tumor (95-02VO16) high grade papillary carcinoma	Pab 55	400x	+
3. Normal ovary (96-08ZO08) control tissue	Pab 55	400x	-
4. Ovary tumor (95-02VO16) high grade papillary carcinoma	Pab 57	400x	+
5. Ovary tumor (9 5 -02VO 16) high grade papillary carcinoma	Pab 57	400x	+
6. Ovary tumor (95-02VO16) high grade papillary carcinoma	Pab 57	400x	+
7. Normal ovary 96-08ZO08) control	Pab 57	400x	-
8. Colon cancer 95-14664) poorly diff. Adenocarcinoma	Pab 55	400x	+
9. Normal colon 9708VO08) control	Pab 55	400x	-
10. Colon cancer 95-14664) poorly diff. Adenocarcinoma	Pab 57	400x	+
11. Colon cancer 95-14664) poorly diff. Adenocarcinoma	Pab 57	400x	+
12. Normal colon 9708VO08) control	Pab 57	400x	-
13. Female breast cancer (97-IOV03a) Invasive mammary carcinoma	Pab 55	400x	+
14. Male breast cancer (no code) mammary carcinoma	Pab 55	400x	+
15. Normal female breast 97-12VO20-3) control	Pab 55	400x	-
16. Female breast cancer 97-IOV03a) Invasive mammary carcinoma	Pab 57	400x	+
17. Male breast cancer (no code) mammary carcinoma	Pab 57	400x	+
18. Normal female breast (97-12VO20-3) control	Pab 57	400x	-
19. Lung cancer (97- 1 OV022-5) poorly diff. NOJ-small cell carcinoma	Pab 55	400x	+
20. Normal lung (98-0 1 VO 11) control	Pab 55		-
21. Lung cancer (97-10VO22-5) poorly diff. NOJ-small cell carcinoma	Pab 57	400x	+
22. Lung cancer (97-10VO22-5) poorly diff. NOJ-small cell carcinoma	Pab 57	400x	+
23. Normal lung (98-0 1 VO 11) control	Pab 57		-

Mouse Tissues:

	Antibody	Magnification	Signal
24. Madison Lung Tumor (MLT) untreated with CM 101	Pab 55		+
25. MLT untreated with CM 101	Pab 55		+
26. Normal mouse lung	Pab 55		-
27. MLT untreated with CM 101	Pab 57		+
28. Normal mouse lung	Pab 57		-

The Pab 55 antibody stains the cells lining a blood vessel in a human ovary cancer tissue section, but such staining is not apparent in cells of normal human ovary tissue (see FIG. 2A and 2B, respectively). Similar results are obtained with the Pab 57 antibody (see FIG. 3A and 3B). As shown in the above table and in FIGS. 2A-3B, antibodies raised to GBS toxin receptor fragments specifically bound to tumor tissues but not normal tissues, suggesting that GBS toxin receptor is expressed in tumor cells but not normal cells.

EXAMPLE 5– DETECTION OF GBS TOXIN RECEPTOR EXPRESSION IN MICE AFFLICTED WITH RHEUMATOID ARTHRITIS

This example shows that GBS toxin receptor can be detected in cells from a mammalian model for rheumatoid arthritis (RA). Mice with collagen-induced arthritis were treated with CM101 or carrier. CM101 reversed the inflammatory damage and inhibited pannus formation. Mouse #8 and #15, which were treated with CM101, and two control mice (not treated with CM101) were sacrificed for immunohistochemistry.

TABLE 10
Immunohistochemistry of Rheumatoid Arthritic Mice

29. No CM 101	Pab 55	+
30. MOUSE 8 - 5' (vessel)	Pab 55	+
31. No CM 101	Pab 57	+
32. MOUSE 15 - 5' (vessel)	Pab 57	+
33. MOUSE 8 - 5' (between joint)	Pab 57	+
34. MOUSE 15 – 5'	Pab 57	+
35. No CM 101 (marrow)	Pab 57	+
36. MOUSE 15 - 5' (marrow)	Pab 57	+

As shown above Pab55 and Pab57 specifically bound to pathologic neovasculature in the pannus, suggesting that GBS toxin receptor is expressed in mice afflicted with rheumatoid arthritis. No binding of CM101 was observed in the normal neovasculature in the growth plate of the joints of the arthritic mice.

EXAMPLE 6 – TARGETED DELIVERY OF A CHIMERIC COMPOUND TO TISSUES EXPRESSING GBS TOXIN RECEPTOR

This example shows the targeted delivery of a chimeric compound to tissues expressing GBS toxin. The chimeric compound is a CM101-biotin conjugate. Mice with Madison Lung Tumors (MLT) are infused intravenously (i.v.) with biotinylated CM 101.

CM101 has been reacted with hydrazinylated biotin to form the biotin hydrazone at the reducing end of the polysaccharide CM101. Briefly, 25 micrograms of lyophilized CM101 is dissolved in 250 μl labeling buffer at 100 mM sodium acetate, 0.02% sodium azide. Aqueous meta-periodate (125 μl of 30 mM) is added and the oxidation is allowed to proceed in the dark for 30 minutes at room temperature. The reaction is terminated by adding 80 mM Na_2SO_3 to the solution. The resultant aldehydes are reacted with 125 μl of 5 mM NHS-LC-Biotin (MW 556.58) for a 1 hour incubation at room temperature to form biotinylated CM101. Excess biotin is removed by dialysis against 1 liter of PBS at 4°C four times. The

product is purified by gel filtration on an Ultrahydrogel 1000 HPLC, lyophilized and stored at -70°C until use.

Tissues are recovered 5 min post infusion with CM101 and subjected to immunohistochemistry. Tumor and normal mouse tissue sections are analyzed for CM 101 binding by both mouse anti-CM101 mAb (7A3), followed by secondary mAb-HRP conjugate (referred to in FIG. 4B as MLT CM101-Biot.5' + McAb), or with avidin (which specifically binds biotin) conjugated with HRP (referred to in FIG. 4A as MLT CM101-Biot.5' + Strep.HRP).

FIGS. 4A-4C depict different sections taken from the same tumor and include a longitudinal view of the same blood vessel approximately in the center of the figures. The dark staining in FIG. 4A shows the localization of the biotin component in the cells lining the blood vessel. Similarly, FIG. 4B depicts the localization of the CM101 component in the cells lining the blood vessel. FIG. 4C is a negative control that was not exposed to CM101. The analysis clearly shows that 7A3 and avidin bind to the same blood vessels in tumor tissue. Thus, biotin has been delivered to the blood vessel of the tumor tissue by virtue of its physical association with a compound (CM101) that binds the GBS toxin receptor.

These studies show that chimeric compounds can be delivered to tissues undergoing pathologic and/or hypoxia-driven angiogenesis or neovascularization. As part of a chimeric compound, cytotoxic molecules can be directed to such tissues, e.g., tumor tissue. The cytotoxic molecule can be coupled directly to a molecule that binds GBS toxin receptor, e.g., GBS toxin. Alternatively, the molecule that binds GBS toxin receptor can be coupled to biotin and the cytotoxic molecule can be coupled to avidin.

EXAMPLE 7 – ENHANCED SENSITIVITY TO GBS-TOXIN-DEPENDENT CYTOTOXICITY OF CELLS EXPRESSING GBS TOXIN RECEPTOR

This example shows the enhanced sensitivity to GBS-toxin-dependent cytotoxicity of cells transfected with the GBS toxin receptor, relative to control cells. Without being bound to a particular theory, the inventors believe that complement binds GBS toxin bound to the GBS toxin receptor on a cell, thereby targeting the cell for killing by white blood cells (WBC).

Human bladder carcinoma cells (ECV cells), are stable transfected with the human GBS toxin receptor gene. The resultant cell line is ECV711. Cells stable transfected with vector alone as referred to as V23. ECV 711 and V23 are seeded in 96-well plates at 5,000 cells/well.

White blood cells are collected from healthy human donors as follows. Blood is collected by standard phlebotomy procedures into heparinized tubes (30 U/ml) and centrifuged at 2000 rpm for 20 min. The interface is carefully transferred to a new tube and washed twice by centrifugation with medium (RPMI-1640). Cells are resuspended in RPMI-1640 supplemented with 5% fetal bovine serum

(FBS) and Interferon-gamma (IFN) at 100 U/ml, and incubated overnight in a 37^{0}C, 5%CO_2 incubator. The cells are then resuspended in fresh medium with 5% FBS.

5,000 cells of the WBC preparation are added to each well containing the transfected cells. CM101 is added to a final concentration of 1μg/ml to the wells together with human serum from matching human donors. The cells are incubated 6 hours at 37 ° C.

Cytotoxicity is assayed by measuring lactate dehydrogenase (LDH) using the Promega's CytoTox 96 Non-Radioactive Assay kit (Nachlas et al. (1960) *Anal. Biochem* 1, 317; Korzeniewski et al. (1983) *J. Immunol. Methods* 64, 313; Decker et al. *J. Immunol. Methods* 115, 61; Brander et al. (1993) *Eur. J. Immunology* 23, 3217; Behl et al. (1994) *Cell* 77, 817; Lappalainen et al. (1994) *Pharm. Research* 11, 1127; Allen et al. (1994) *Promega Notes* 45, 7; Sinensky et al. (1995) *Toxicol. Letters* 75, 02; Moravec (1994) *Promega Notes* 45, 11). Percent cytotoxicity is calculated as recommended by the manufacturer's instructions. The results are shown in Table 11.

Table 11

Cytotoxicity	ECV 711	V 23
WBC, IFN, C3, -CM101	29.1%	27.5%
WBC, IFN, C3, +CM101	40.45%	22.46%

There is an increase in cytotoxicity of 39% when the ECV 711 cells are incubated with CM101, WBC and human serum (source of C3) compared to cells incubated without CM101. Control cells transfected with vector alone, V23, do not show a CM101 dependent increase in cytotoxicity.

All publications and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

The invention now being fully described, it will be apparent to one of ordinary skill in the art that many changes and modifications can be made thereto without departing from the spirit or scope of the appended claims.